

OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 07:16:57 ; Search time 5792.24 Seconds
(without alignments)
11720.367 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtggttaaggttgca.....ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1784.4	95.8	1788	9	AY401283	AY401283 Homo sapi
2	1783	95.7	3186	3	BC036783	BC036783 Homo sapi
3	1739.4	93.4	1788	9	AY401284	AY401284 Pan trogl
4	1544.4	82.9	1788	9	AY401285	AY401285 Mus muscu
5	1521	81.6	2534	3	AK044636	AK044636 Mus muscu
6	971	52.1	1589	3	CNSLT1IBJ	BX248763 human ful
7	899.2	48.3	938	5	BX374548	BX374548 BX374548
8	805	43.2	887	4	BI913344	BI913344 603178823

9	784.8	42.1	2922	9	AY398961	AY398961 Homo sapi
10	768.2	41.2	939	5	BX347210	BX347210 BX347210
11	755	40.5	2922	9	AY398963	AY398963 Mus muscu
12	739.8	39.7	792	4	BI522813	BI522813 603175911
13	737.8	39.6	916	5	BX368185	BX368185 BX368185
14	710.4	38.1	4374	3	AK035163	AK035163 Mus muscu
15	708.4	38.0	894	5	BX390204	BX390204 BX390204
16	673.2	36.1	775	5	BQ770745	BQ770745 UI-M-FI0-
17	638	34.2	3573	3	AK048160	AK048160 Mus muscu
18	635.4	34.1	2516	9	AY408693	AY408693 Homo sapi
19	607	32.6	2881	9	AY398962	AY398962 Pan trogl
20	598.6	32.1	944	5	BX368184	BX368184 BX368184
c 21	579.2	31.1	753	9	AG462634	AG462634 Mus muscu
22	574.6	30.8	752	7	CF532853	CF532853 UI-M-GH0-
c 23	553.6	29.7	1062	9	CNS04DXR	AL286344 Tetraodon
24	503.8	27.0	588	7	CF533347	CF533347 UI-M-FY0-
25	497	26.7	704	7	CF729293	CF729293 UI-M-HD0-
26	483.2	25.9	851	5	BX325851	BX325851 BX325851
27	456.8	24.5	676	2	BB280958	BB280958 BB280958
28	412.4	22.1	503	8	BZ211245	BZ211245 CH230-426
c 29	407.4	21.9	499	8	BH349372	BH349372 CH230-32M
30	403.4	21.7	2515	9	AY408695	AY408695 Mus muscu
31	397.2	21.3	911	5	BU901346	BU901346 AGENCOURT
32	368.4	19.8	1139	5	BX355386	BX355386 BX355386
33	363.6	19.5	829	9	CC501501	CC501501 CH240_339
34	359	19.3	569	4	BI906774	BI906774 603064517
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36	341.2	18.3	830	5	BU747974	BU747974 CH3#016_H
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c 38	338	18.1	1020	9	CNS03Y28	AL265769 Tetraodon
39	327.4	17.6	2472	9	AY408694	AY408694 Pan trogl
c 40	320	17.2	384	8	AZ258968	AZ258968 RPCI-23-1
c 41	304.4	16.3	818	8	BZ163286	BZ163286 CH230-276
42	303	16.3	462	1	AL712986	AL712986 DKFZp686J
43	298.4	16.0	767	7	CR426134	CR426134 CR426134
44	295.8	15.9	693	2	BB648018	BB648018 BB648018
c 45	294.2	15.8	551	9	FR0052027	AL688306 Fugu rubr

ALIGNMENTS

RESULT 1

AY401283

LOCUS AY401283 1788 bp DNA linear GSS 15-DEC-2003

DEFINITION Homo sapiens SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY401283

VERSION AY401283.1 GI:39757272

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1788)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES Location/Qualifiers
 source 1. .1788
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
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 /gene="SLC8A3"
 /locus_tag="HCM0839"
 ORIGIN
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 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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 Db 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
 Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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 Qy 121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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 Db 241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300
 Qy 301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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 Db 301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
 Qy 361 ACCAGCACAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420
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 Db 361 ACCAGCACAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
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Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
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Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
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Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
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Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
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Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
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Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
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Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260

Qy 1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
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Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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 Db 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 1786

RESULT 2

BC036783

LOCUS BC036783 3186 bp mRNA linear HTC 19-NOV-2003

DEFINITION Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3, mRNA (cDNA clone IMAGE:5732743), with apparent retained intron.

ACCESSION BC036783

VERSION BC036783.1 GI:23331089

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3186)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 3186)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (23-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 79 Row: j Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17865803
This clone has the following problem: retained intron.

FEATURES Location/Qualifiers

source 1. .3186
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/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 95.7%; Score 1783; DB 3; Length 3186;
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Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db    558 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 617

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Qy     121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180
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Qy     181 CCAATCTGGTACCCGGAGAAACCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
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Db	1818	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1877
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1878	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1937
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1938	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1997
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1998	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2057
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	2058	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	2117
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620

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Db      2118 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 2177
Qy      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
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Db      2178 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 2237
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db      2238 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2297
Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
|||||
Db      2298 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2353
Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db      2354 GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2394

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RESULT 3

AY401284

LOCUS AY401284 1788 bp DNA linear GSS 15-DEC-2003

DEFINITION Pan troglodytes SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY401284

VERSION AY401284.1 GI:39757273

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..1788

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

gene <1..>1788

/gene="SLC8A3"
/locus_tag="HCM0839"

ORIGIN

Query Match 93.4%; Score 1739.4; DB 9; Length 1788;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1746; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        ||||||||||| |||||||||||||||||||||||||||||||||||||||
Db     61 TTTGTGCTCTTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
        ||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy    241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db    241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCG 300

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACGATTAAGAAACCCAATGGAGAA 360

Qy    361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCC 420
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Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
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Db    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCACCTA 600

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db	721		TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781		ATGCACAAAAAGTACCGCACAGATAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841		CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841		CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901		CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901		CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961		AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961		AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCTAAT	1020
Qy	1021		TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021		TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGGATCCAAGCCACTCGT	1080
Qy	1081		ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081		ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141		TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141		TCCAGCATGANNGAGGTGCACACCGATGANNCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201		GACCCATGTTCTTACCAAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201		GACCCATGTTCTTACCAATGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261		AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261		AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTNNNGCC	1320
Qy	1321		AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321		AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381		CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381		CAGAAGGAGTTCTCCGTAGGCATAATTNNNGACGACATTTNNNAGGAGGATGAACACTTN	1440
Qy	1441		TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441		NNNNNAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGNCTCCA	1500
Qy	1501		GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501		GCAATANNCAACAGTNNNNCTTGCCTCGGGCTGTNNTAGCCTCCCCTTGTGTNGCCACA	1560
Qy	1561		GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620

Db 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620

Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
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Db 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680

Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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Db 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 1786

RESULT 4

AY401285

LOCUS AY401285 1788 bp DNA linear GSS 15-DEC-2003

DEFINITION Mus musculus SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY401285

VERSION AY401285.1 GI:39757274

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..1788

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

gene <1..>1788

/gene="SLC8A3"

/locus_tag="HCM0839"

ORIGIN

Query Match 82.9%; Score 1544.4; DB 9; Length 1788;

Best Local Similarity 91.5%; Pred. No. 0;
Matches 1635; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTACGGCTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACT	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATTGTCTTCGAGCAGAGGCTGGTGACTCGGGGGATGTGCCCAGT	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	121	GCAGGGCAGAACAATGAGTCCTGTTCGGGGTCATCAGACTGCAAGGAGGGTGTCATTTTG	180
Qy	181	CCAATCTGGTACCCGGAACCCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTATCCAGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTTCTTGGGGTGTCATCATTGCTGACCGATTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATTACTTCCCAAGAGAGGGAAGTGACCATCAAGAAGCCCAATGGAGAG	360
Qy	361	ACCAGCACAACCCTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	361	ACCAGCACAACCTACAATTTCGGGTATGGAATGAACTGTCTCCAATCTGACCCTGATGGCC	420
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGCTCTTCTGCTCCAGAGATTCTCCTGTCTTTAATTGAGGTGTGTGGTCACGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCATCTACCATCGTTGGCAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTATGTGATCCCAGATGGGGAGACTCGAAAGATCAAGCACCTG	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCGTCACGGCTGCTTGGAGCATCTTCGCCTACATTTGGCTCTATATGATC	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCTCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTTACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCCGTGTGTGTCCTGCTGGCTTGGGTGGCAGATAAGCGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840

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 Db 1201 GACCCATGTTCTTATCAGTGCCTGGAGAACTGTGGAGCTGTCTCCTGACCGTGGTGAGG 1260
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 Db 1261 AAAGGGGGAGATATATCCAAGACCATGTACGTGGACTACAAAACAGAGGACGGCTCCGCC 1320
 Qy 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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 Db 1321 AATGCAGGGGCAGACTATGAGTTCACAGAGGGCACTGTGGTTCTGAAGCCAGGAGAGACC 1380
 Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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 Db 1381 CAGAAGGAGTTCTCTGTGGGCATCATTGATGATGACATTTTTGAGGAGGATGAACACTTC 1440
 Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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 Db 1441 TTTGTGAGGCTGAGCAATGTCCGTGTAGAAGAGGAGCAGCTGGCGGAGGGGATGCTCCCA 1500
 Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
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 Db 1501 GCAATACTCAATAGTCTTCCCTTGCCTCGGGCTGTCTGGCCTCCCCTTGTGTGGCCACA 1560
 Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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 Db 1561 GTAACCATCTTGGATGATGACCATGCAGGAATTTTCACTTTTGAATGTGATACTATTCAT 1620
 Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT 1680
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 Db 1621 GTCAGTGAAAGTATTGGTGTATGGAAGTCAAGGTTTTGAGGACATCAGGTGCCAGGGGC 1680

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Qy      1681 ACAGTCATCGTCCCCTTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db      1681 ACAGTCATCGTCCCCTTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGTGGCGAGGACTTT 1740

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1741 GAAGATGCATATGGGGAGCTGGAGTTCAAGAATGATGAAACAGTGT 1786

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RESULT 5

AK044636

LOCUS AK044636 2534 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930029A02 product:solute carrier family 8 (sodium/calcium exchanger), member 3, full insert sequence.

ACCESSION AK044636

VERSION AK044636.1 GI:26336660

KEYWORDS HTC; CAP trapper.

SOURCE *Mus musculus* (house mouse)

ORGANISM *Mus musculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE

4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE

5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2534)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2534

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/strain="C57BL/6J"

/db_xref="FANTOM_DB:A930029A02"

/db_xref="taxon:10090"

/clone="A930029A02"

/tissue_type="retina"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

CDS 713. .>2533

/note="unnamed protein product; putative solute carrier family 8 (sodium/calcium exchanger), member 3 (MGD|MGI:107976, GB|NM_080440, evidence: BLASTN, 99%, match=2394)"

/codon_start=1

/protein_id="BAC32013.1"

/db_xref="GI:26336661"

/translation="MCPVQGRTMSPVRGHQTARRVSFCQLWYPENPSLGDKIARVIVY FVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTL

Db	1203	TGCGAGTCTTCTTCGTACGGCTGCTTGGAGCATCTTCGCTACATTTGGCTCTATATGA	1262
Qy	659	TTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCT	718
Db	1263	TCCTGGCAGTCTTCTCTCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTTACTCTCTTCT	1322
Qy	719	TCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAAT	778
Db	1323	TCTTTCCCGTGTGTGTCTGCTGGCTTGGGTGGCAGATAAGCGACTGCTCTTCTACAAAT	1382
Qy	779	ACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTG	838
Db	1383	ACATGCACAAAAAATACCGCACAGATAAACACCGAGGAATTATCATTGAGACAGAGGGTG	1442
Qy	839	ACCACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGA	898
Db	1443	ACCACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCTCACTTTCTAGATGGGA	1502
Qy	899	ACCTGGTGGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTTC	958
Db	1503	ACTTTACACCTTTGGAAGGAAAGGAGGTAGATGAATCTCGCAGGGAAATGATCCGGATTTC	1562
Qy	959	TCAAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCA	1018
Db	1563	TAAAGGATCTGAAACAAAAACACCCAGAAAAGGACCTAGATCAGCTGGTGGAGATGGCCA	1622
Qy	1019	ATTACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTC	1078
Db	1623	ATTACTATGCTCTTTCCCATCAACAGAAGAGCCGTGCTTCTACCGCATCCAAGCCACCC	1682
Qy	1079	GTATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGG	1138
Db	1683	GGATGATGACTGGTGCAGGCAATATACTTAAGAAGCATGCAGCCGAGCAAGCCAAGAAGA	1742
Qy	1139	CCTCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCT	1198
Db	1743	CCTCCAGCATGAGCGAGGTGCATACCGATGAGCCGGAGGACTTTGCCTCTAAGGTCTTCT	1802
Qy	1199	TTGACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGA	1258
Db	1803	TTGACCCATGTTCTTATCAGTGCCTGGAGAACTGTGGAGCTGTCTCCTGACCGTGGTGA	1862
Qy	1259	GGAAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTG	1318
Db	1863	GGAAAGGGGGAGATATATCCAAGACCATGTACGTGGACTACAAAACAGAGGACGGCTCCG	1922
Qy	1319	CCAATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGA	1378
Db	1923	CCAATGCAGGGGCAGACTATGAGTTCACAGAGGGCACTGTGGTTCTGAAGCCAGGAGAGA	1982
Qy	1379	CCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACT	1438
Db	1983	CCCAGAAGGAGTTCTCTGTGGGCATCATTGATGATGACATTTTTGAGGAGGATGAACACT	2042
Qy	1439	TCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTC	1498
Db	2043	TCTTTGTGAGGCTGAGCAATGTCCGTGTAGAAGAGGAGCAGCTGGCGGAGGGGATGCTCC	2102

Qy	1499	CAGCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCA	1558
Db	2103	CAGCAATACTCAATAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCA	2162
Qy	1559	CAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTC	1618
Db	2163	CAGTAACCATCTTGGATGATGACCATGCAGGAATTTTCACTTTTGAATGTGATAACCATTC	2222
Qy	1619	ATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGG	1678
Db	2223	ATGTCAGTGAAAGTATTGGTGTTATGGAAGTCAAGGTTTGTAGGACATCAGGTGCCAGGG	2282
Qy	1679	GTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACT	1738
Db	2283	GCACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGTGCGAGGACT	2342
Qy	1739	TTGAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTATGTGACAGACAGG	1798
Db	2343	TTGAAGATGCATATGGGGAGCTGGAGTTCAGAATGATGAAAC----AGTGA AACATA	2398
Qy	1799	AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841
Db	2399	AGGGTTAAATAGTAGATGAGGAGGAGTACGAGAGGCAAGAGA	2441

RESULT 6

LOCUS	CNSLT1IBJ	1589 bp	mRNA	linear	HTC 18-JUN-2003
DEFINITION	human full-length cDNA 5-PRIME end of clone CS0DB006YD18 of Neuroblastoma of Homo sapiens (human).				
ACCESSION	BX248763				
VERSION	BX248763.1 GI:28375580				
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1589)				
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue				
REFERENCE	2 (bases 1 to 1589)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-FEB-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				

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source      1. .1589
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            /clone="CS0DB006YD18"
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            /note="end : 5-PRIME~Cot 10-normalized~vector pCMVSPORT_6"
CDS         619. .>1589
            /note="unnamed protein product"
            /codon_start=1
            /protein_id="CAD66570.1"
            /db_xref="GI:28375581"
            /translation="MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQN
NESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASI
EVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGF
IAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLY
MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE
TEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDL"

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ORIGIN

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Query Match          52.1%; Score 971; DB 3; Length 1589;
Best Local Similarity 100.0%; Pred. No. 4.8e-267;
Matches 971; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db      619 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 678

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db      679 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 738

Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      739 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 798

Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      799 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 858

Qy      241 TTTGTGGCCCTGATATACATGTTCTTGGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db      859 TTTGTGGCCCTGATATACATGTTCTTGGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 918

Qy      301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db      919 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 978

Qy      361 ACCAGCACAACCACTATTCCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db      979 ACCAGCACAACCACTATTCCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 1038

Qy      421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db      1039 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1098

Qy      481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

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Db      1099 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 1158
Qy      541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db      1159 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1218
Qy      601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
      |||
Db      1219 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1278
Qy      661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
      |||
Db      1279 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1338
Qy      721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db      1339 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1398
Qy      781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db      1399 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1458
Qy      841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db      1459 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1518
Qy      901 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db      1519 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1578
Qy      961 AAGGATCTGAA 971
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Db      1579 AAGGATCTGAA 1589

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RESULT 7

BX374548

LOCUS BX374548 938 bp mRNA linear EST 23-APR-2004

DEFINITION BX374548 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens cDNA clone CS0DB006YD18 5-PRIME, mRNA sequence.

ACCESSION BX374548

VERSION BX374548.2 GI:46558208

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 938)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30438490.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7256.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DB006DB09_DB1287_2&c=7256.r.

FEATURES

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source          Location/Qualifiers
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS0DB006YD18"
                /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
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                /note="1st strand cDNA was primed with a NotI-oligo(dT)
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                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

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Query Match          48.3%; Score 899.2; DB 5; Length 938;
Best Local Similarity 97.8%; Pred. No. 1.7e-246;
Matches 918; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

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Qy      687 CCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTG 746
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Qy      747 GGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAA 806
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Db      60 GGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAA 119

Qy      807 ACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATGG 866
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Db      120 ACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATGG 179

Qy      867 GAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAGT 926
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Db      180 GAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAGT 239

Qy      927 GGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAGA 986
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Db      240 GGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAGA 299

Qy      987 GAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAACAGAA 1046
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Db      300 GAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAACAGAA 359

Qy      1047 GAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCT 1106
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Db      360 GAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCT 419

Qy      1107 GAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGA 1166
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Db      420 GAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGA 479

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Qy 1167 TGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGA 1226
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 Db 480 TGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGA 539

Qy 1227 GAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCAT 1286
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 Db 540 GAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCAT 599

Qy 1287 GTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCAC 1346
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 Db 600 GTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCAC 659

Qy 1347 AGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAAT 1406
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 Db 660 AGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAAT 719

Qy 1407 TGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCAT 1466
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 Db 720 TGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGNTAGGTTGAGCAATGTCCGCAT 779

Qy 1467 AGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCC 1526
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 Db 780 AGAGGAGGAGCAGCCAGAGGAGGGGATGCCTNNCAGCATATTCAAACAGTCTTCCCTTGCC 839

Qy 1527 TCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGC 1586
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 Db 840 TCGGGCTGTCCTAGCCTNCCCTTGNGTGGNCACAGTTACCATCTTGGATGATGACCATGC 899

Qy 1587 AGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG 1625
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 Db 900 NAGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG 938

RESULT 8

BI913344

LOCUS BI913344 887 bp mRNA linear EST 16-OCT-2001

DEFINITION 603178823F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243308 5', mRNA sequence.

ACCESSION BI913344

VERSION BI913344.1 GI:16177710

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 887)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11613 row: m column: 05
High quality sequence stop: 782.

FEATURES
source Location/Qualifiers
1. .887
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5243308"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 43.2%; Score 805; DB 4; Length 887;
Best Local Similarity 98.0%; Pred. No. 2e-219;
Matches 836; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

Qy 916 GGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 975
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Db 1 GGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 60
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Db 61 AAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCC 120
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Db 121 CACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCA 180
Qy 1096 GGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAG 1155
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Db 181 GGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAG 240
Qy 1156 GTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC 1215
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Db 241 GTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC 300
Qy 1216 CAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATG 1275
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Db 301 CAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATG 360
Qy 1276 TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 1335
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Db 361 TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 420
Qy 1336 TATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC 1395

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Db      421 TATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC 480
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Db      481 GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC 540
Qy      1456 AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT 1515
Db      541 AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT 600
Qy      1516 CTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT 1575
Db      601 CTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT 660
Qy      1576 GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATT 1635
Db      661 GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTA-T 719
Qy      1636 GGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGTACAGTCATCGTCCCC 1695
Db      720 GGTGTAATGGAGGTCAAGGTTCTGCGGACATCATGTGCCCCGGGGTACAGTCATCGTCCCC 779
Qy      1696 TTT-AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGG 1754
Db      780 TTTGAGGACAGGAGAAGGGACAGCCAAGGCTGCACGCTAAGGACTTGAAGACCCATATGC 839
Qy      1755 GGAGTTGGAATTC 1767
Db      840 GGAGTTGGAATTC 852

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RESULT 9

AY398961

LOCUS AY398961 2922 bp DNA linear GSS 15-DEC-2003

DEFINITION Homo sapiens SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY398961

VERSION AY398961.1 GI:39754950

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2922)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2922)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

TITLE Adams,M.D. and Cargill,M.
 Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES Location/Qualifiers
 source 1. .2922
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 gene <1..>2922
 /gene="SLC8A1"
 /locus_tag="HCM0065"

ORIGIN

Query Match 42.1%; Score 784.8; DB 9; Length 2922;
 Best Local Similarity 68.3%; Pred. No. 2.1e-213;
 Matches 1165; Conservative 0; Mismatches 502; Indels 39; Gaps 4;

Qy	109	GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAG	168
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Qy	169	GGTGTTCATCCTGCCAATCTGGTACCCGGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG	228
Db	172	GGGGTGATTTTGCCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA	231
Qy	229	GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGAC	288
Db	232	GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT	291
Qy	289	CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA	348
Db	292	CGGTTTCATGTCCTCTATAGAAGTCATCACATCTCAAGAAAAAGAAATAACCATAAAGAAA	351
Qy	349	CCCAATGGAGAAACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTG	408
Db	352	CCCAATGGAGAGACCACCAAGACAACCTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG	411
Qy	409	ACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT	468
Db	412	ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTCAGTAATTGAAGTGTGT	471
Qy	469	GGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC	528
Db	472	GGCCATAACTTCACTGCAGGAGACCTCGGTCCTAGCACCATCGTGGGAAGTGCTGCATTC	531
Qy	529	AACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG	588
Db	532	AATATGTTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG	591
Qy	589	ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG	648
Db	592	ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG	651
Qy	649	CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC	708

Db	652	CTTTACATTATTTTGTCTGTCATATCTCCTGGTGTGTGGAGGTCTGGGAAGGTTTGCTT	711
Qy	709	ACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC	768
Db	712	ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTTCGCTTGGGTAGCGGATAGGAGACTTCTG	771
Qy	769	TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG	828
Db	772	TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA	831
Qy	829	ACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATGAAT	879
Db	832	CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT	891
Qy	880	TCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAG-----	921
Db	892	TCTCATGTTGAAAATTTCTTAGATGGTGCTCTGGTTCTGGAGGTGGATGAGAGGGACCAA	951
Qy	922	GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC	981
Db	952	GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACCTAAGCAGAAGCAT	1011
Qy	982	CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAA	1041
Db	1012	CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG	1071
Qy	1042	CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT	1101
Db	1072	CAAAAAGTAGAGCATTTTATCGCATTCAGCTACTCGCCTCATGACTGGAGCTGGCAAC	1131
Qy	1102	ATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC	1161
Db	1132	ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCAGCATGCACGAGGTCAAC	1191
Qy	1162	ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG	1218
Db	1192	ACTGAAGTGACTGAAAATGACCCTGTTAGTAAGATCTTCTTTGAACAAGGGACATATCAG	1251
Qy	1219	TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCA	1278
Db	1252	TGTCTGGAGAACTGTGGTACTGTGGCCCTTACCATTATCCGCAGAGGTGGTGATTGACT	1311
Qy	1279	AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT	1338
Db	1312	AACACTGTGTTTGTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT	1371
Qy	1339	GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG	1398
Db	1372	GAATTTACTGAAGGAAGTGTGGTGTTTAAGCCTGGTGATACCCAGAAGGAAATCAGAGTG	1431
Qy	1399	GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT	1458
Db	1432	GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTCCTTGTGCATCTCAGCAAT	1491
Qy	1459	GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT	1518

Db	1492	GTCAAAGTATCTTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC-----CAATCAT	1542
Qy	1519	CCCTTGCGCTCGGGCTGTCCTAGCCTCCCCTTGTTGTGGCCACAGTTACCATCTTGGATGAT	1578
Db	1543	GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAAC TATTTTTGATGAT	1602
Qy	1579	GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGT	1638
Db	1603	GACCACGCAGGCATTTTTACTTTTGAGGAACCTGTGACTCATGTGAGTGAGAGCATTGGC	1662
Qy	1639	GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGTACAGTCATCGTCCCCTTT	1698
Db	1663	ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT	1722
Qy	1699	AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAG	1758
Db	1723	AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTTGAGGACACTTGTGGAGAG	1782
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/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

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Query Match          41.2%; Score 768.2; DB 5; Length 939;
Best Local Similarity 95.6%; Pred. No. 7.7e-209;
Matches 854; Conservative 0; Mismatches 33; Indels 6; Gaps 6;

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Qy      165 GGAGGGTGTTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGC 224
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Db      80  GGAGGGTGTTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGC 139

Qy      225 CAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGC 284
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Db      140 CAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGC 199

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Db      200 TGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAA 259

Qy      345 GAAACCCAATGGAGAAACCAGCACAAACCACTATTCCGGTCTGGAATGAACTGTCTCCAA 404
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Db      260 GAAACCCAATGGAGAAACCAGCACAAACCACTATTCCGGTCTGGAATGAACTGTCTCCAA 319

Qy      405 CCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGT 464
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Db      320 CCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGT 379

Qy      465 GTGTGGTCATGGGTTCAATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGC 524
        |||
Db      380 GTGTGGTCATGGGTTCAATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGC 439

Qy      525 CTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCG 584
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Db      440 CTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCG 499

Qy      585 CAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACAT 644
        |||
Db      500 CAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACAT 559

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Db      560 CTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGG-AGGCCT 618

Qy      705 CCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACT 764
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 Qy 825 AGAGACAGAGGGTGACCACCCTAAGGGCATTTGAGATGGATGGGAAAATGATGAATTCCCA 884
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 Db 738 AGAGACAGAGGGTGACCACCCTAGGGGCTTTGGGATGGGTGGGAAAAGGATGAATTCCCA 797
 Qy 885 TTTTCTAGATGGGAACCTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGT-CCCGCAGAG 943
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 Db 798 TTTTCTAGGAGGGAAACCTGTGCCCCCTGAAGGGAAGAAAGTGGATTAATCCCCGCAGAG 857
 Qy 944 AGATGATCCGGATTCTC-AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTT 995
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RESULT 11

AY398963

LOCUS AY398963 2922 bp DNA linear GSS 15-DEC-2003

DEFINITION Mus musculus SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY398963

VERSION AY398963.1 GI:39754952

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2922)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2922)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .2922
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 gene <1..>2922
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ORIGIN

Query Match 40.5%; Score 755; DB 9; Length 2922;
Best Local Similarity 67.8%; Pred. No. 7.8e-205;
Matches 1134; Conservative 0; Mismatches 500; Indels 39; Gaps 4;

Qy	142	TGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTCCTGCCAATCTGGTACCCGGAGAAC	201
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Qy	202	CCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATG	261
Db	205	CCATCTTTTGGGGACAAAATTGCTAGAGCAACTGTGTATTTTGTGGCCATGGTCTACATG	264
Qy	262	TTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCT	321
Db	265	TTCTTGGAGTTTCTATTATTGCAGACCGGTTTATGTCTCTATAGAGGTCATCACCTCT	324
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Qy	442	ATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTATTGCTGGTGATCTGGGACCT	501
Db	445	ATTCTCCTGTGAGTCATTGAAGTGTGCGGCCATAACTTCACCGCAGGGGACCTGGGTCCC	504
Qy	502	TCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTTGGCATCTGTGTCTAC	561
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Qy	562	GTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCT	621
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Qy	622	GCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGT	681
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Qy	682	GTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTTCCAGTGTGTGTCCTTCTG	741
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Qy	742	GCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAGTACCGCACA	801
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Qy	802	GACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCC-----TAAGGGC	852
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Qy	853	ATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTG	912
Db	865	ATCGAAATGGATGGGAAAGTGGTCAACTCTCATGTTGACAATTTCTTAGATGGGGCTCTG	924

Qy 913 G-----AAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGG 954
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 Db 925 GTTTTGAAGTTGATGAGAGGGACCAAGATGATGAGGAAGCCAGGCGTGAGATGGCAAG 984

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 Db 985 ATTCTGAAGGAACCTTAAGCAGAAGCATCCTGAGAAAAGAAATTGAGCAATTAATAGAATTA 1044

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Qy 1075 ACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAG 1134
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 Db 1165 AAGGCTGTCAGTATGCATGAAGTCAACATGGAATGGCTGAAAACGACCCAGTCAGTAAG 1224

Qy 1192 GTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACA 1251
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 Db 1225 ATCTTCTTTGAGCAAGGAACATACCAGTGTCTAGAGAACTGTGGTACTGTGGCCCTCACC 1284

Qy 1252 GTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGAT 1311
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 Db 1285 ATTATGCGCAGAGGGGGCGACTTGAGCACCACCTGTGTTTGTGACTTCAGGACAGAAGAC 1344

Qy 1312 GGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCA 1371
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 Db 1345 GGCACAGCCAATGCTGGGTCTGATTATGAATTCACGGAAGGGACTGTGATCTTCAAACCA 1404

Qy 1372 GGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGAT 1431
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 Db 1405 GGGGAGACCCAGAAGGAAATCAGAGTTGGCATCATTGATGATGATATCTTTGAAGAAGAT 1464

Qy 1432 GAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGG 1491
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 Db 1465 GAAAACCTCCTTGTGCATCTTAGCAATGTCAGAGTCTCTTCAGATGTTTCAGAAGATGGC 1524

Qy 1492 ATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGT 1551
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Qy 1552 GTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGAT 1611
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 Db 1576 ACTGCCACCATAACCATTTTTGATGATGACCATGCAGGCATCTTTACATTTGAGGAACCC 1635

Qy 1612 ACTATTCATGTGAGTGAAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGT 1671
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 Db 1636 GTGACTCACGTGAGCGAGAGCATTGGCATCATGGAGGTGAAGGTTTGAAGACCTCTGGA 1695

Qy 1672 GCCCGGGGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGT 1731
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 Db 1696 GCTCGAGGAAATGTTATCATTCCCTACAAAACCTATTGAAGGCACAGCCCGAGGTGGAGGG 1755

Qy 1732 GAGGACTTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGT 1784

Db 1756 GAAGACTTTGAGGACACCTGTGGAGAGCTCGAATTCCAGAACGATGAAATAGT 1808

RESULT 12

BI522813

LOCUS BI522813 792 bp mRNA linear EST 29-AUG-2001

DEFINITION 603175911F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240066 5', mRNA sequence.

ACCESSION BI522813

VERSION BI522813.1 GI:15347605

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 792)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11605 row: f column: 03

High quality sequence stop: 778.

FEATURES

source

Location/Qualifiers

1. .792

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/clone="IMAGE:5240066"

/lab_host="DH10B"

/clone_lib="NIH_MGC_121"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 39.7%; Score 739.8; DB 4; Length 792;

Best Local Similarity 98.7%; Pred. No. 1.1e-200;

Matches 767; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Qy 993 CTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCAACAGAAGAGCCG 1052

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Qy          1053 CGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAA 1112
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Db          61 CGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAA 120
Qy          1113 ACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCC 1172
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Db          121 ACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCC 180
Qy          1173 TGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAAGT 1232
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Db          181 TGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAAGT 240
Qy          1233 TGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGT 1292
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Db          241 TGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGT 300
Qy          1293 GGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGG 1352
              |||
Db          301 GGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGG 360
Qy          1353 CACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGA 1412
              |||
Db          361 CACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGA 420
Qy          1413 CGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGA 1472
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Db          421 CGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGA 480
Qy          1473 GGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGC 1532
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Db          481 GGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGC 540
Qy          1533 TGTCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCAT 1592
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RESULT 13

BX368185

LOCUS BX368185 916 bp mRNA linear EST 26-APR-2004

DEFINITION BX368185 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CS0DD006YJ07 5-PRIME, mRNA sequence.

ACCESSION BX368185

VERSION BX368185.2 GI:46572003
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 916)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 8, 2003 this sequence version replaced gi:30445119.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 7256.r
 For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAA006ZD07_CS00533_2&c=7256.r

FEATURES Location/Qualifiers
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 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 39.6%; Score 737.8; DB 5; Length 916;
 Best Local Similarity 95.1%; Pred. No. 4.2e-200;
 Matches 827; Conservative 0; Mismatches 33; Indels 10; Gaps 6;

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Db	166	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	225
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	226	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	285

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861

REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4374)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES

source

Location/Qualifiers

1. .4374

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/dev_stage="12 days embryo"

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281..3046

/note="SODIUM/CALCIUM EXCHANGER 2 PRECURSOR

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100%length, match=2763)
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ORIGIN

Query Match 38.1%; Score 710.4; DB 3; Length 4374;

Best Local Similarity 65.9%; Pred. No. 6.1e-192;

Matches 1092; Conservative 0; Mismatches 536; Indels 30; Gaps 3;

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Qy 1204 CCATGTTCTTACAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAA 1263
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RESULT 15

BX390204

LOCUS BX390204 894 bp mRNA linear EST 28-APR-2004

DEFINITION BX390204 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CS0DD006YJ07 5-PRIME, mRNA sequence.

ACCESSION BX390204

VERSION BX390204.2 GI:46834875

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 894)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30461412.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAG010ZA11_CS00945_1&c=7256.r

ORIGIN

Qy	30	CTCTGCCTTCCTCCATTTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGC	89
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
3: gb_in:*
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10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1784.6	95.8	3812	6	AX496815	AX496815 Sequence
5	1784.4	95.8	2534	9	HSNCX22	X93017 Homo sapien
6	1783	95.7	2781	6	AX299471	AX299471 Sequence
7	1783	95.7	2782	6	AX476818	AX476818 Sequence
8	1783	95.7	2837	9	HSA304853	AJ304853 Homo sapi
9	1783	95.7	2966	6	AX480881	AX480881 Sequence
10	1783	95.7	5250	9	AF510501	AF510501 Homo sapi
11	1783	95.7	5268	9	AF510502	AF510502 Homo sapi
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21	1544	82.9	3435	10	AF453257	AF453257 Mus muscu
22	1527	82.0	4854	10	RNU53420	U53420 Rattus norv
23	1526.8	82.0	247722	2	AC099080	AC099080 Rattus no
24	1331.4	71.5	3838	9	HSA508602	AJ508602 Homo sapi
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26	938.6	50.4	77568	2	AC139418	AC139418 Homo sapi
c 27	913.2	49.0	77568	2	AC139418	AC139418 Homo sapi
c 28	895.8	48.1	248965	2	CR361558	CR361558 Danio rer
29	810.6	43.5	4087	4	BOVEXCHANG	L06438 Bos taurus
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32	799.4	42.9	3150	4	CATSCE	L35846 Felis catus
33	796.2	42.7	3292	4	OCU52665	U52665 Oryctolagus
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35	792.8	42.6	1832	9	AF109888	AF109888 Macaca mu
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40	785.2	42.1	1836	6	CQ178689	CQ178689 Sequence
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42	785.2	42.1	1836	6	CQ264524	CQ264524 Sequence
43	785.2	42.1	1836	6	CQ301620	CQ301620 Sequence
44	785.2	42.1	1836	6	CQ338834	CQ338834 Sequence
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ALIGNMENTS

RESULT 1

AX496813

LOCUS AX496813 1863 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 3 from Patent WO02059316.
 ACCESSION AX496813
 VERSION AX496813.1 GI:23342336
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hilbun, E. and Friddle, C.J.

TITLE Human ion exchanger proteins and polynucleotides encoding the same

JOURNAL Patent: WO 02059316-A 3 01-AUG-2002;

LEXICON GENETICS INC (US)

FEATURES Location/Qualifiers

source 1. .1863

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/mol_type="unassigned DNA"

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ORIGIN

Query Match 100.0%; Score 1863; DB 6; Length 1863;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

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Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

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Db 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy 121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180

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Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
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Qy	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
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Db      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
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Db      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860
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Db      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860
Qy      1861 TGA 1863
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Db      1861 TGA 1863

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RESULT 2

AF510503

LOCUS AF510503 5146 bp mRNA linear PRI 30-OCT-2002

DEFINITION Homo sapiens Na⁺/Ca²⁺ exchanger isoform 3 splice variant 4 (SLC8A3) mRNA, complete cds; alternatively spliced.

ACCESSION AF510503

VERSION AF510503.1 GI:24421224

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5146)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE The human SLC8A3 gene and the tissue-specific Na⁽⁺⁾/Ca⁽²⁺⁾ exchanger 3 isoforms

JOURNAL Gene 298 (1), 1-7 (2002)

MEDLINE 22294016

PUBMED 12406570

REFERENCE 2 (bases 1 to 5146)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE Direct Submission

JOURNAL Submitted (09-MAY-2002) Department of Biology, Univ. of Padova, via G. Colombo, Padova, PD 35131, Italy

FEATURES Location/Qualifiers

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ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      875 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 934

Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db      935 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 994

Qy      241 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db	1055	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	1114
Qy	361	ACCAGCACAAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	1115	ACCAGCACAAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	1174
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1235	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1294
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTGCCTACATCTGGCTCTATATGATT	660
Db	1355	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTGCCTACATCTGGCTCTATATGATT	1414
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
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Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
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Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1835	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1894

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Qy	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
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Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
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Db	2075	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	2134
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Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
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Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
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Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	2375	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	2434
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
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Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA	1800
Db	2495	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA	2554
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG	1860
Db	2555	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG	2614
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Db	2615	TGA	2617

RESULT 3

AX496811

LOCUS AX496811 2766 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 1 from Patent WO02059316.
 ACCESSION AX496811
 VERSION AX496811.1 GI:23342335
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Hilbun, E. and Friddle, C.J.
 TITLE Human ion exchanger proteins and polynucleotides encoding the same
 JOURNAL Patent: WO 02059316-A 1 01-AUG-2002;
 LEXICON GENETICS INC (US)
 FEATURES Location/Qualifiers
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ORIGIN

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 Best Local Similarity 98.5%; Pred. No. 0;
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Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
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Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
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Db	481	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
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Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCACTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCACTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380


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Db      1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCCTGAAGCCAGGAGAGACC 1380
Qy      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTTAGCCTCCCCTTGTGTGGCCACA 1560
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Db      1501 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTTAGCCTCCCCTTGTGTGGCCACA 1560
Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
Qy      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
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Db      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796
Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db      1797 GGT TAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

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RESULT 4

AX496815

LOCUS AX496815 3812 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 5 from Patent WO02059316.

ACCESSION AX496815

VERSION AX496815.1 GI:23342337

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hilbun,E. and Friddle,C.J.

TITLE Human ion exchanger proteins and polynucleotides encoding the same

JOURNAL Patent: WO 02059316-A 5 01-AUG-2002;

LEXICON GENETICS INC (US)

FEATURES

Location/Qualifiers

source

1. .3812

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 95.8%; Score 1784.6; DB 6; Length 3812;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
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Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	678	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	737
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	738	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	797
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	798	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	857
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	858	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	917
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	918	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	977
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	978	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	1037
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	1038	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	1097
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1098	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1157
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1218	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1277
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1278	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1337
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1338	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1397

Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1398	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1457
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAAC	900
Db	1458	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAAC	1517
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1518	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1577
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1578	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1637
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1638	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1697
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1698	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1757
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1758	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1817
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1818	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1877
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1878	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1937
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1938	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1997
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1998	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2057
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2058	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2117
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	2118	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	2177
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	2178	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	2237
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680

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Db      2238 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT 2297
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
      |||
Db      2298 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357
Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db      2358 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2413
Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db      2414 GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2454

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RESULT 5

HSNCX22

LOCUS HSNCX22 2534 bp DNA linear PRI 12-NOV-2000

DEFINITION Homo sapiens partial SCL8A3 gene for solute carrier family 8 (sodium/calcium exchanger), member 3 (SCL8A3), exon 2.

ACCESSION X93017

VERSION X93017.1 GI:1067133

KEYWORDS SLC8A3 gene; sodium-calcium exchanger.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS Kraev,A., Chumakov,I. and Carafoli,E.

TITLE The organization of the human gene NCX1 encoding the sodium-calcium exchanger

JOURNAL Genomics 37 (1), 105-112 (1996)

MEDLINE 97079665

PUBMED 8921376

REFERENCE 2 (bases 1 to 2534)

AUTHORS Kraev,A.S.

TITLE Direct Submission

JOURNAL Submitted (14-NOV-1995) A.S. Kraev, Swiss Federal Institute of Technology, Laboratory of Biochemistry III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND

COMMENT Similar to X91213.

FEATURES

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exchanger), member 3"
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ORIGIN

Query Match 95.8%; Score 1784.4; DB 9; Length 2534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
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Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	403	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	462
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	463	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	522
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	523	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	582
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	583	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	642
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	643	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	702
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	703	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	762
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	763	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	822
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	823	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	882
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	883	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	942
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	943	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1002
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1003	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1062

Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1063	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1122
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1123	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1182
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATCCCATTTTCTAGATGGGAAC	900
Db	1183	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATCCCATTTTCTAGATGGGAAC	1242
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1243	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1302
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1303	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1362
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1363	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1422
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1423	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1482
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1483	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1542
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
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Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1603	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1662
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
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Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1723	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1782
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1783	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1842
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
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Db      1963 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 2022
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db      2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082
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Db      2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128

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RESULT 6

AX299471

LOCUS AX299471 2781 bp DNA linear PAT 26-NOV-2001

DEFINITION Sequence 1 from Patent WO0183744.

ACCESSION AX299471

VERSION AX299471.1 GI:17129228

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Wilm, C.

TITLE Natrium-calcium exchanger protein

JOURNAL Patent: WO 0183744-A 1 08-NOV-2001;

MERCK PATENT GmbH (DE)

FEATURES Location/Qualifiers

source

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CDS

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ORIGIN

Query Match 95.7%; Score 1783; DB 6; Length 2781;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACATATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCC	420
Db	361	ACCAGCACAACCACATATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCC	420
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780

Db	721	 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620

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Db      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
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Db      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGTATGTGACAGACAGGAA 1800
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Db      1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAAC----TGTGAAAACCATAAG 1796
Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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RESULT 7

AX476818

LOCUS AX476818 2782 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 1 from Patent WO0233086.

ACCESSION AX476818

VERSION AX476818.1 GI:22216098

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Merkulov,G.V., Ketchum,K.A., Shao,W., Yan,C., di Francesco,V. and
Beasley,E.M.

TITLE Isolated human transporter proteins, nucleic acid molecules
encoding human transporter proteins, and uses thereof

JOURNAL Patent: WO 0233086-A 1 25-APR-2002;
PE Corporation (NY) (US)

FEATURES

source Location/Qualifiers
1. .2782
/organism="Homo sapiens"
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ORIGIN

Query Match 95.7%; Score 1783; DB 6; Length 2782;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Db      70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129
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Db	190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	249
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
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Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	369
Qy	361	ACCAGCACAAACCACTATTCCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	370	ACCAGCACAAACCACTATTCCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCCTTATGGCC	429
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	430	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	549
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Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
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Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
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Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020

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Qy 1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db 1270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1329

Qy 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db 1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1389

Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db 1510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1569

Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
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Db 1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1629

Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
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Db 1630 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1689

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Db 1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
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Db 1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1805

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Db 1806 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846

RESULT 8

HSA304853

LOCUS HSA304853 2837 bp mRNA linear PRI 06-JUN-2001

DEFINITION Homo sapiens mRNA for sodium/calcium exchanger, SCL8A3, alternative splice form B (SCL8A3 gene).

ACCESSION AJ304853

VERSION AJ304853.1 GI:14330384

KEYWORDS alternative splicing; form B; SCL8A3 gene; SCL8A3 protein; Sodium/calcium exchanger.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Gabellini,N.

TITLE Characterization of the human SCL8A3 gene for solute carrier family 8, member 3 (sodium/calcium exchanger)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2837)

AUTHORS Bortoluzzi,S.

TITLE Direct Submission

JOURNAL Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and Department of Biological Chemistry, University of Padova, via G. Colombo 3, 35131 PADOVA, ITALY

FEATURES

source

Location/Qualifiers

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CDS

63. .2837

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/function="sodium/calcium exchanger"

/note="alternative splice form B (exons 2, 4, 5, 9, 10, 11, 12)"

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ORIGIN

Query Match 95.7%; Score 1783; DB 9; Length 2837;
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Db	183	ACAGGGCAGAACAATGAGTCCTGTTTCAAGGTCATCGGACTGCAAGGAGGGTGTCTCCTG	242
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
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Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
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Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	363	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	422
Qy	361	ACCAGCACAACCACTATTGGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	423	ACCAGCACAACCACTATTGGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	482
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Db	483	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	542
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	543	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	602
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	603	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	662
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Db	843	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	902
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Db	1323	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1382
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
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Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1443	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1502
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1503	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1562
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Db      1563 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1622
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Db      1623 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACCTTTTGAATGTGATACTATTCAT 1682
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RESULT 9

AX480881

LOCUS AX480881 2966 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 41 from Patent WO0246415.

ACCESSION AX480881

VERSION AX480881.1 GI:22217538

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Lee,E.A., Baughn,M.R., Yue,H., Ding,L., Raumann,B.E., Hafalia,A.J.,
Khan,F.A., Nguyen,D.B., Elliott,V.S., Ramkumar,J., Walia,N.K.,
Ison,C.H., Lu,Y., Gandhi,A.R., Warren,B.A., Duggan,B.M.,
Tribouley,C.M., Burford,N., Lu,D.A., Lal,P.G., Yao,M.G., Xu,Y.,
Bruns,C.M., Thangavelu,K., Swarnakar,A., Tang,Y.T., Azimzai,Y.,
Thornton,M., Arvizu,C. and Policky,J.L.

TITLE Transporters and ion channels

JOURNAL Patent: WO 0246415-A 41 13-JUN-2002;

Incyte Genomics, Inc. (US)

FEATURES

source

Location/Qualifiers

1. .2966

/organism="Homo sapiens"

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ORIGIN

Query Match 95.7%; Score 1783; DB 6; Length 2966;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Db	201	 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	260
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	261	 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	320
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	321	 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	380
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	381	 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	440
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	441	 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	500
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	501	 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	560
Qy	361	ACCAGCACAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	561	 ACCAGCACAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	620
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	681	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	740
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	741	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	800
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	801	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	860
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	861	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	920
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	921	 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	980
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	981	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1040
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900

Db	1041	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCCATTTTCTAGATGGGAAC	1100
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1101	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1160
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1161	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1220
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1221	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1280
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1281	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1340
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1341	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1400
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
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Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1461	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1520
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1521	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1580
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1581	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1640
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1641	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1700
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1701	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1760
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1761	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1820
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1821	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1880
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1881	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1940

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ORIGIN

Query Match 95.7%; Score 1783; DB 9; Length 5250;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	755	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	814
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	815	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	874
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
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Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	935	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	994
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	995	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	1054
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
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Qy	361	ACCAGCACAACCACTATTCCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCC	420
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Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
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Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1475	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1534
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1535	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1594
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Db	1595	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	1654
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
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Db	1775	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1834
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Db	1835	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1894
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Db	1895	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1954
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Db	1955	GACCCATGTTCTTACCAAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	2014
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Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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 Db 2435 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2494

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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 Db 2495 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2550

Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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RESULT 11

AF510502

LOCUS AF510502 5268 bp mRNA linear PRI 30-OCT-2002

DEFINITION Homo sapiens Na⁺/Ca²⁺ exchanger isoform 3 splice variant 3 (SLC8A3) mRNA, complete cds; alternatively spliced.

ACCESSION AF510502

VERSION AF510502.1 GI:24421222

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo...

REFERENCE 1 (bases 1 to 5268)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE The human SLC8A3 gene and the tissue-specific Na⁽⁺⁾/Ca⁽²⁺⁾ exchanger 3 isoforms

JOURNAL Gene 298 (1), 1-7 (2002)

MEDLINE 22294016

PUBMED 12406570

REFERENCE 2 (bases 1 to 5268)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE Direct Submission

JOURNAL Submitted (09-MAY-2002) Department of Biology, Univ. of Padova, via

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FEATURES             Location/Qualifiers
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ORIGIN

Query Match 95.7%; Score 1783; DB 9; Length 5268;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	755	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	814
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	815	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	874
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTATCCTG	180

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Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
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Db	1595	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1654
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1655	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1714
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1715	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1774

Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1775	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1834
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1835	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1894
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1895	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1954
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1955	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	2014
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	2015	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	2074
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	2075	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	2134
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	2135	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2194
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2195	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2254
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	2255	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	2314
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	2315	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	2374
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	2375	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	2434
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2435	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2494
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA	1800
Db	2495	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG	2550
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841
Db	2551	GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA	2591

RESULT 12

CQ736275

LOCUS CQ736275 1788 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 22209 from Patent WO02068579.

ACCESSION CQ736275

VERSION CQ736275.1 GI:42330964

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.

TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof

JOURNAL Patent: WO 02068579-A 22209 06-SEP-2002;

PE Corporation (NY) (US)

FEATURES Location/Qualifiers

source

1. .1788

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 95.7%; Score 1782.8; DB 6; Length 1788;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps . 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAAACCACTATTGGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAAACCACTATTGGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420

Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260

Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT	1786
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT	1786

RESULT 13

AX476820

LOCUS	AX476820	126512 bp	DNA	linear	PAT 12-AUG-2002
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DEFINITION Sequence 3 from Patent WO0233086.

ACCESSION AX476820

VERSION AX476820.1 GI:22216099

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Merkulov,G.V., Ketchum,K.A., Shao,W., Yan,C., di Francesco,V. and Beasley,E.M.

TITLE Isolated human transporter proteins, nucleic acid molecules encoding human transporter proteins, and uses thereof

JOURNAL Patent: WO 0233086-A 3 25-APR-2002; PE Corporation (NY) (US)

FEATURES Location/Qualifiers

source 1. .126512

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 95.7%; Score 1782.8; DB 6; Length 126512;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	2010	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	2069
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	2070	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	2129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	2130	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	2189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	2190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	2249
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	2250	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	2309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	2310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	2369
Qy	361	ACCAGCACAACCACTATTCCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	2370	ACCAGCACAACCACTATTCCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	2429
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	2430	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	2489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	2490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	2549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	2550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	2609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	2610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	2669
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	2670	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	2729

Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	2730	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	2789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	2790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	2849
Qy	841	CACCCTAAGGGCATTTAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Db	2850	CACCCTAAGGGCATTTAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	2909
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	2910	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	2969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	2970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	3029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	3030	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	3089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	3090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	3149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	3150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	3209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	3210	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	3269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	3270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	3329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	3330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	3389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	3390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	3449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	3450	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	3509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	3510	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	3569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620

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Db      3570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 3629
Qy      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
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Db      3630 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 3689
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
      |||
Db      3690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 3749
Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTAT 1786
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Db      3750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGT 3795

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RESULT 14

AF508982

LOCUS AF508982 145118 bp DNA linear PRI 24-OCT-2002

DEFINITION Homo sapiens Na⁺/Ca²⁺ exchanger isoform 3 (SLC8A3) gene, promoter region and complete cds.

ACCESSION AF508982

VERSION AF508982.1 GI:22087482

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 145118)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE The human SLC8A3 gene and the tissue-specific Na⁺/Ca²⁺ exchanger 3 isoforms

JOURNAL Gene 298 (1), 1-7 (2002)

REFERENCE 2 (bases 1 to 145118)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE Control of the Na⁺/Ca²⁺ exchanger 3 promoter by cAMP and Ca²⁺ in differentiating neurons

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 145118)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE Direct Submission

JOURNAL Submitted (02-MAY-2002) Department of Biology, University of Padova, via G. Colombo 3, Padova, PD 35131, Italy

FEATURES Location/Qualifiers

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source      1. .145118
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             /db_xref="taxon:9606"
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gene        1. .145118
             /gene="SLC8A3"
promoter    1. .263
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5'UTR join(264. .955,20853. .20914) /gene="SLC8A3"

CDS join(20915. .22698,128396. .128499,133522. .133539, 137221. .137345,138228. .138327,140293. .140568, 143012. .143388) /gene="SLC8A3" /note="NCX3; expressed in excitable cells of brain, retina, and skeletal muscle" /codon_start=1 /product="Na+/Ca2+ exchanger isoform 3" /protein_id="AAM90955.1" /db_xref="GI:22087483" /translation="MAWLRQLQPLTSAFLHFGLVTFVLFNLGLRAEAGGSGDVPSTGQN NESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFRMASI EVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGF IAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLY MILAVFSPGVVQVWEGLLTLFFFVPCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE TEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPEKDLQ LVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE DFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTE GTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPL PRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRVTSARGTVIVPF RTVEGTAKGGGEDFEDTYGELEFKNDET VKTIRVKIVDEEEYERQENFFIALGEPKWM ERGISALLLSPDVTDRKLTMEEEEAKRIAEMGKPVLGHPKLEVIIIESEYFKTTVDK LIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLT VFWK VLFACVPPTEYCHGWACFAVSILIIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFG TSVPDTFASKAAALQDVYADASIGNVTGSNAVNVLGIGLAWSVAAIYWALQGQEFHV SAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATWLFVSLWLLYIL FATLEAYCYIKGF"

3'UTR 143389. .145118 /gene="SLC8A3"

polyA_signal 145089. .145094 /gene="SLC8A3"

ORIGIN

Query Match 95.7%; Score 1782.8; DB 9; Length 145118;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	20915	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	20974
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	20975	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	21034
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	21035	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	21094

Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	21095	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	21154
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
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Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
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Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC	480
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
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RESULT 15

AC009607

LOCUS AC009607 146055 bp DNA linear HTG 04-MAY-2001
 DEFINITION Homo sapiens clone RP11-1I11, WORKING DRAFT SEQUENCE, 31 unordered pieces.

ACCESSION AC009607
 VERSION AC009607.3 GI:8072446
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 146055)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens, clone RP11-1I11
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 146055)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
 Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
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 Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
 Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
 Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
 TITLE Direct Submission
 JOURNAL Submitted (28-AUG-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On May 25, 2000 this sequence version replaced gi:7321520.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L1464
 Center clone name: 1_I_11
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 99% of reads
 Sequencing vector: Plasmid; n/a; %0.0% of reads
 0.776287932251235Chemistry: Dye-primer-amersham; 6% of reads
 Chemistry: Dye-terminator Big Dye; 94% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 126247 bases at least Q40
 Consensus quality: 134710 bases at least Q30
 Consensus quality: 138332 bases at least Q20
 Insert size: 160000; agarose-fp
 Insert size: 143055; sum-of-contigs
 Quality coverag.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 31 contigs. The true order of the pieces
 * is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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ORIGIN

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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26	785.2	42.1	1836	4	ABA64480	Aba64480 Human foe
27	785.2	42.1	1836	4	AAI44657	Aai44657 Probe #13
28	785.2	42.1	1836	4	ABA31619	Aba31619 Probe #10
29	785.2	42.1	1836	4	AAK12937	Aak12937 Human bra
30	785.2	42.1	1836	4	ABS38231	Abs38231 Human liv
31	785.2	42.1	1836	6	ABS12734	Abs12734 Human gen
32	784.8	42.1	2814	4	AAH57377	Aah57377 Human hea
33	784.8	42.1	3250	12	ADP21419	Adp21419 Gene SLC8
34	784.8	42.1	5438	5	ABV24305	Abv24305 Human pro
35	765.8	41.1	3037	10	ADB59225	Adb59225 Toxicity-
36	692.4	37.2	4282	9	AAL55587	Aal55587 Human 465
37	692.4	37.2	4291	3	AAC75706	Aac75706 Human ORF
38	503.4	27.0	505	12	ACH73341	Ach73341 Human gen
39	494	26.5	551	12	ACH70908	Ach70908 Human gen
40	366	19.6	366	12	ACH84609	Ach84609 Human gen
41	334.4	17.9	507	12	ACH70808	Ach70808 Human gen
42	319	17.1	4546	4	ABL09809	Abl09809 Drosophil
43	319	17.1	24221	4	ABL09808	Abl09808 Drosophil
44	180	9.7	180	12	ACH84511	Ach84511 Human gen
45	164.2	8.8	459	4	AAI10174	Aai10174 Probe #10

ALIGNMENTS

RESULT 1

ABQ78862

ID ABQ78862 standard; cDNA; 1863 BP.

XX

AC ABQ78862;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #2 cDNA.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;

KW gene; ss; chromosome 14.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1. .1863
 FT /*tag= a
 FT /product= "Ion exchanger protein 2"
 XX
 PN WO200259316-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001817.
 XX
 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 DR P-PSDB; ABB81914.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Disclosure; Page 39-40; 42pp; English.
 XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence encodes a NHIEP of the invention
 XX
 SQ Sequence 1863 BP; 464 A; 426 C; 514 G; 459 T; 0 U; 0 Other;

Query Match 100.0%; Score 1863; DB 6; Length 1863;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180

Db	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020

Qy	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG	1860
Db	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG	1860

Qy 1861 TGA 1863
|||
Db 1861 TGA 1863

RESULT 2

ABQ78861

ID ABQ78861 standard; cDNA; 2766 BP.

XX

AC ABQ78861;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;

KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;

KW gene; ss; chromosome 14.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .2766

FT /*tag= a

FT /product= "Ion exchanger protein 1"

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

DR P-PSDB; ABB81913.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.

XX

PS Claim 1; Page 36-37; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence encodes a NHIEP of the invention

SQ Sequence 2766 BP; 655 A; 678 C; 760 G; 673 T; 0 U; 0 Other;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780

Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620

Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTATGTGACAGACAGGAA	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAAC---TGTGAAAACCATAAG	1796
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841
Db	1797	GGTTAAATAGTAGATGAGGAGGAATACGAAAGGCAGAGA	1837

XX
PS Disclosure; Page; 42pp; English.

XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)

XX
SQ Sequence 2766 BP; 654 A; 678 C; 761 G; 673 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 2766;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540

Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440

```

      |||
Db      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC 1440
Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
      |||
Db      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
      |||
Db      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
      |||
Db      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
Qy      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT 1680
      |||
Db      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT 1680
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
      |||
Db      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
      |||
Db      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796
Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
      |||
Db      1797 GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

```

RESULT 4

ABQ78866

ID ABQ78866 standard; cDNA; 2769 BP.

XX

AC ABQ78866;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA A/G+GCA mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW gene; ss; mutant.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT mutation replace(1889,A)

FT /*tag= a

FT mutation replace(2113. .2115,-)

FT /*tag= b

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001817.
 XX
 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Disclosure; Page; 42pp; English.
 XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence represents a mutant form of a NHIEP of the invention. Note: The
 CC present sequence is not shown in the specification but is derived from
 CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)
 XX
 SQ Sequence 2769 BP; 655 A; 679 C; 762 G; 673 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 2769;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300

Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200

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Db      1141  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1200
Qy      1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
Db      1201  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1260
Qy      1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
Db      1261  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1320
Qy      1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
Db      1321  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1380
Qy      1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
Db      1381  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1440
Qy      1441  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
Db      1441  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1500
Qy      1501  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
Db      1501  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1560
Qy      1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
Db      1561  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1620
Qy      1621  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
Db      1621  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1680
Qy      1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
Db      1681  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1740
Qy      1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
Db      1741  ||||||||||||||||||||||||||||||||||||||||||||| ||||| ||| | 1796
Qy      1801  GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
Db      1797  |||| ||| ||| ||||| | | ||||
Db      1797  GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

```

RESULT 5

ABQ78865

ID ABQ78865 standard; cDNA; 2769 BP.

XX

AC ABQ78865;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA GCA mutant.

Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960

Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1796

Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
 | | | | | | | | | | | | | | |
 Db 1797 GGT TAA AATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

RESULT 6

ADH42314

ID ADH42314 standard; DNA; 2778 BP.

XX

AC ADH42314;

XX

DT 25-MAR-2004 (first entry)

XX

DE Novel human nucleic acid NOV55g.

XX

KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;
 KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;
 KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;
 KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;
 KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
 KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
 KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX

OS Homo sapiens.

XX

PN WO2003102159-A2.

XX

PD 11-DEC-2003.

XX

PF 04-JUN-2003; 2003WO-US017573.

XX

PR 04-JUN-2002; 2002US-0385490P.

PR 04-JUN-2002; 2002US-0385615P.

PR 04-JUN-2002; 2002US-0385755P.

PR 05-JUN-2002; 2002US-0386041P.

PR 06-JUN-2002; 2002US-0386355P.

PR 06-JUN-2002; 2002US-0386357P.

PR 06-JUN-2002; 2002US-0386447P.

PR 06-JUN-2002; 2002US-0386459P.

PR 06-JUN-2002; 2002US-0386465P.

PR 06-JUN-2002; 2002US-0386864P.

PR 07-JUN-2002; 2002US-0386701P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0387078P.

PR 07-JUN-2002; 2002US-0387081P.

PR 07-JUN-2002; 2002US-0387083P.

PR 10-JUN-2002; 2002US-0387429P.

PR 10-JUN-2002; 2002US-0387540P.

PR 10-JUN-2002; 2002US-0387866P.

PR 11-JUN-2002; 2002US-0387606P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387659P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 12-JUN-2002; 2002US-0388432P.
PR 12-JUN-2002; 2002US-0388479P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389604P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390144P.
PR 19-JUN-2002; 2002US-0390209P.
PR 25-JUN-2002; 2002US-0391726P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402268P.
PR 12-AUG-2002; 2002US-0402822P.
PR 13-AUG-2002; 2002US-0403458P.
PR 15-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403732P.
PR 26-AUG-2002; 2002US-0406182P.
PR 12-SEP-2002; 2002US-0410085P.
PR 13-SEP-2002; 2002US-0410505P.
PR 23-SEP-2002; 2002US-0412955P.
PR 30-SEP-2002; 2002US-0415195P.
PR 23-OCT-2002; 2002US-0420627P.
PR 23-OCT-2002; 2002US-0420718P.
PR 24-OCT-2002; 2002US-0420852P.
PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.
PR 05-NOV-2002; 2002US-0423748P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;
PI Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE;
PI Millet I, Padigar M, Patturajan M, Peyman JA, Qian X, Rastelli L;
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;
PI Wolenc AR, Zhong M, Zhong H;

XX

DR WPI; 2004-053467/05.

DR P-PSDB; ADH42315.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.

XX

PS Claim 20; SEQ ID NO 867; 1503pp; English.

XX

CC The invention relates to 566 new isolated human polypeptides and their

CC encoding genes, sequences that are at least 95% identical to these or
 CC sequences comprising one or more conservative substitutions in these. The
 CC polypeptide, polynucleotide and antibodies against the polypeptides are
 CC useful in diagnosing, treating or preventing NOVX-associated disorders,
 CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
 CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
 CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
 CC The nucleic acids are further used as hybridization probes, in chromosome
 CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
 CC polypeptides are also useful as vaccines. This sequence represents an
 CC example of the nucleic acid sequence of the invention.

XX

SQ Sequence 2778 BP; 656 A; 684 C; 764 G; 674 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 12; Length 2778;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	10	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	69
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	70	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	130	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	249
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	250	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	369
Qy	361	ACCAGCACAACCCTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	370	ACCAGCACAACCCTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	429
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	430	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	609

Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	669
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	670	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	729
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	730	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	909
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	910	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1030	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1449

Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
 |||
 Db 1450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1509
 Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
 |||
 Db 1510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1569
 Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
 |||
 Db 1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1629
 Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
 |||
 Db 1630 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1689
 Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 |||
 Db 1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749
 Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
 |||
 Db 1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACATAAG 1805
 Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
 |||
 Db 1806 GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846

RESULT 7

ADH42306

ID ADH42306 standard; DNA; 2778 BP.

XX

AC ADH42306;

XX

DT 25-MAR-2004 (first entry)

XX

DE Novel human nucleic acid NOV55c.

XX

KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;
 KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;
 KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;
 KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;
 KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
 KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
 KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX

OS Homo sapiens.

XX

PN WO2003102159-A2.

XX

PD 11-DEC-2003.

XX

PF 04-JUN-2003; 2003WO-US017573.

XX

PR 04-JUN-2002; 2002US-0385490P.

PR 04-JUN-2002; 2002US-0385615P.

PR 04-JUN-2002; 2002US-0385755P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386355P.
PR 06-JUN-2002; 2002US-0386357P.
PR 06-JUN-2002; 2002US-0386447P.
PR 06-JUN-2002; 2002US-0386459P.
PR 06-JUN-2002; 2002US-0386465P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0386701P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0387078P.
PR 07-JUN-2002; 2002US-0387081P.
PR 07-JUN-2002; 2002US-0387083P.
PR 10-JUN-2002; 2002US-0387429P.
PR 10-JUN-2002; 2002US-0387540P.
PR 10-JUN-2002; 2002US-0387866P.
PR 11-JUN-2002; 2002US-0387606P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387659P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 12-JUN-2002; 2002US-0388432P.
PR 12-JUN-2002; 2002US-0388479P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389604P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390144P.
PR 19-JUN-2002; 2002US-0390209P.
PR 25-JUN-2002; 2002US-0391726P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402268P.
PR 12-AUG-2002; 2002US-0402822P.
PR 13-AUG-2002; 2002US-0403458P.
PR 15-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403732P.
PR 26-AUG-2002; 2002US-0406182P.
PR 12-SEP-2002; 2002US-0410085P.
PR 13-SEP-2002; 2002US-0410505P.
PR 23-SEP-2002; 2002US-0412955P.
PR 30-SEP-2002; 2002US-0415195P.
PR 23-OCT-2002; 2002US-0420627P.
PR 23-OCT-2002; 2002US-0420718P.
PR 24-OCT-2002; 2002US-0420852P.
PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.
PR 05-NOV-2002; 2002US-0423748P.
XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;
PI Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE;
PI Millet I, Padigar M, Patturajan M, Peyman JA, Qian X, Rastelli L;
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;
PI Wolenc AR, Zhong M, Zhong H;

XX

DR WPI; 2004-053467/05.

DR P-PSDB; ADH42307.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.

XX

PS Claim 20; SEQ ID NO 859; 1503pp; English.

XX

CC The invention relates to 566 new isolated human polypeptides and their
CC encoding genes, sequences that are at least 95% identical to these or
CC sequences comprising one or more conservative substitutions in these. The
CC polypeptide, polynucleotide and antibodies against the polypeptides are
CC useful in diagnosing, treating or preventing NOVX-associated disorders,
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC The nucleic acids are further used as hybridization probes, in chromosome
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC polypeptides are also useful as vaccines. This sequence represents an
CC example of the nucleic acid sequence of the invention.

XX

SQ Sequence 2778 BP; 656 A; 684 C; 764 G; 674 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 12; Length 2778;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 60
|
Db 10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 69

Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
|
Db 70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129

Qy 121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
|
Db 130 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 189

Qy 181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
|
Db 190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249

Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	250	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	369
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	370	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	429
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	430	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	669
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	670	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	729
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	730	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	909
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	910	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1030	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1089

Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1449
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1450	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1510	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1570	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1629
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1630	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1689
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1690	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1749
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA	1800
Db	1750	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG	1805
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841
Db	1806	GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA	1846

RESULT 8

ABQ78863

ID ABQ78863 standard; cDNA; 3812 BP.

XX

AC ABQ78863;
 XX
 DT 09-OCT-2002 (first entry)
 XX
 DE Human ion exchanger protein cDNA #3.
 XX
 KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW gene; ss; chromosome 14.
 XX
 OS Homo sapiens.
 XX
 PN WO200259316-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001817.
 XX
 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Disclosure; Page 41-42; 42pp; English.
 XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence encodes a NHIEP of the invention, with regions of flanking
 CC sequence
 XX
 SQ Sequence 3812 BP; 860 A; 1059 C; 1041 G; 852 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 3812;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 677
 Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	738	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	797
Qy	181	CCAATCTGGTACCCGGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	798	CCAATCTGGTACCCGGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	857
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	858	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	917
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	918	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	977
Qy	361	ACCAGCACAAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	978	ACCAGCACAAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	1037
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	1038	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	1097
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1098	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1157
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1158	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1217
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1218	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1277
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1278	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1337
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1338	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1397
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1398	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1457
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1458	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1517
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1518	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1577

Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1578	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1637
Qy	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1638	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1697
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1698	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1757
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1758	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1817
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1818	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1877
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1878	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1937
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCGAAGCCAGGAGAGACC	1380
Db	1938	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCGAAGCCAGGAGAGACC	1997
Qy	1381	CAGAAGGAGTTCCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1998	CAGAAGGAGTTCCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2057
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2058	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2117
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	2118	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	2177
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	2178	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	2237
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	2238	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	2297
Qy	1681	ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2298	ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2357
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Db	2358	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	2413
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841

Db 2414 GGT TAA AATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2454

RESULT 9

ACC00414

ID ACC00414 standard; cDNA; 2534 BP.

XX

AC ACC00414;

XX

DT 04-JUL-2003 (first entry)

XX

DE Human 69039 coding sequence.

XX

KW Human; 69039; neuroprotective; gene therapy; haematopoietic disorder;

KW Na⁺/Ca²⁺ exchanger; ion transporter; neural tissue;

KW neurological disorder; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 343..2130

FT /*tag= a

FT /product= "Human 69039"

XX

PN WO2003029410-A2.

XX

PD 10-APR-2003.

XX

PF 27-SEP-2002; 2002WO-US030817.

XX

PR 28-SEP-2001; 2001US-0325737P.

XX

PA (MILL-) MILLENIUM PHARM INC.

XX

PI Carroll JM;

XX

DR WPI; 2003-381617/36.

DR P-PSDB; ABR40134.

XX

PT Identifying a nucleic acid molecule associated with a disorder for
PT preparing a composition for treating hematopoietic or neurological
PT disorder by detecting the presence of a nucleic acid molecule in the
PT sample that is amplified.

XX

PS Claim 1; Page 109-110; 133pp; English.

XX

CC The present sequence is the coding sequence for human 69039, a novel
CC Na⁺/Ca²⁺ exchanger family member (ion transporter). 69039 was shown to be
CC expressed in human haematopoietic cells, e.g. CD34-expressing progenitor
CC cells as well as in neural tissues, e.g. brain cortex and hypothalamus.
CC 69039 may therefore be used for preparing a composition for treating
CC haematopoietic or neurological disorder

XX

SQ Sequence 2534 BP; 602 A; 595 C; 644 G; 693 T; 0 U; 0 Other;

Query Match

95.8%; Score 1784.4; DB 10; Length 2534;

Db	1123	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1182
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Db	1183	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	1242
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1243	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1302
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1303	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1362
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1363	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1422
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1423	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1482
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1483	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1542
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1543	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1602
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1603	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1662
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1663	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1722
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1723	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1782
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1783	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1842
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1843	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1902
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1903	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1962
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1963	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	2022

QY 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 |||
 Db 2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

QY 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
 |||
 Db 2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128

RESULT 10

ABA04756

ID ABA04756 standard; cDNA; 2781 BP.

XX

AC ABA04756;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3, cDNA.

XX

KW Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
 KW cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
 KW myocarditis; pulmonary hypertension; cardiotoxicity; cardiant; Vaccine;
 KW coronary heart disease; renal failure; ischaemic disorder;
 KW Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .2781

FT /*tag= a

FT /partial

FT /product= "Human natrium(+)-calcium(2+) exchanger form 3
 protein, HNCX3"

FT /note= "No stop codon given"

XX

PN WO200183744-A2.

XX

PD 08-NOV-2001.

XX

PF 30-APR-2001; 2001WO-EP004886.

XX

PR 02-MAY-2000; 2000EP-00109080.

XX

PA (MERE) MERCK PATENT GMBH.

XX

PI Wilm C;

XX

DR WPI; 2002-041493/05.

DR P-PSDB; AAM47745.

XX

PT New polypeptide, useful as vaccines for inducing immune response against
 PT diseases such as myocardial infarction, arrhythmia, ischemic disorders,
 PT renal disorders in mammal.

XX

PS Claim 4; Page 34-38; 41pp; English.

XX

CC The present sequence is the coding sequence for human Sodium(+)-Calcium
CC (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome
CC 14. HNCX3 and its coding sequence are useful for treating acute and
CC chronic cardiac failure of different aetiologies, myocardial infarction,
CC cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,
CC cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,
CC acute and chronic renal failure, ischaemic disorders of skeletal muscle
CC and ischaemic brain disorders of different aetiologies

XX

SQ Sequence 2781 BP; 658 A; 678 C; 765 G; 680 T; 0 U; 0 Other;

Query Match 95.7%; Score 1783; DB 6; Length 2781;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

```
Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
        |||
Db      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        |||
Db     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy    121 ACAGGGCAGAACAATGAGTCCTGTT CAGGGTCATCGGACTGCAAGGAGGGTGT CATCCTG 180
        |||
Db    121 ACAGGGCAGAACAATGAGTCCTGTT CAGGGTCATCGGACTGCAAGGAGGGTGT CATCCTG 180

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
        |||
Db    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy    241 TTTGTGGCCCTGATATACATGTT CCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
        |||
Db    241 TTTGTGGCCCTGATATACATGTT CCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
        |||
Db    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy    361 ACCAGCACAACCACTATT CGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420
        |||
Db    361 ACCAGCACAACCACTATT CGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy    421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480
        |||
Db    421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
        |||
Db    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
        |||
Db    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
        |||
```

Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTTAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTTAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTTACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTTACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500

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Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
          |||
Db      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
          |||
Db      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
          |||
Db      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680

Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
          |||
Db      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
          |||
Db      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
          |||
Db      1797 GGTATAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

```

RESULT 11

ABN83428

ID ABN83428 standard; cDNA; 2782 BP.

XX

AC ABN83428;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein coding sequence.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
 KW spleen; testis; leukocyte; foetal brain; chromosome 14; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 10. .2775

FT /*tag= a

FT /product= "Human transporter"

XX

PN WO200233086-A2.

XX

PD 25-APR-2002.

XX

PF 17-OCT-2001; 2001WO-US032152.

XX

PR 17-OCT-2000; 2000US-0240836P.

PR 13-MAR-2001; 2001US-00804474.

XX

PA (PEKE) PE CORP NY.

XX

PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;

PI Beasley EM;

XX

DR WPI; 2002-479677/51.

DR P-PSDB; ABB83246.

XX

PT Human transporter peptide related to sodium/calcium exchanger subfamily
PT for identifying modulators useful for treating a disease or condition
PT mediated by human transporter protein.

XX

PS Claim 4; Fig 1; 200pp; English.

XX

CC The present sequence is the coding sequence of a human transporter
CC protein, which is related to the sodium/calcium exchanger subfamily.
CC Experimental data indicates expression of the transporter gene in humans
CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal
CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR

XX

SQ Sequence 2782 BP; 655 A; 685 C; 766 G; 676 T; 0 U; 0 Other;

Query Match 95.7%; Score 1783; DB 6; Length 2782;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

```
Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
      |||
Db      10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
      |||
Db     70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
      |||
Db    130 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 189

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
      |||
Db    190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249

Qy    241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300
      |||
Db    250 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 309

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
      |||
Db    310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369

Qy    361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCC 420
      |||
Db    370 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCC 429

Qy    421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
      |||
Db    430 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 489

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
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Db	490	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	550	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	610	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	669
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	670	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	729
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	730	 TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	790	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	850	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	909
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	910	 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC	969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	970	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1030	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1090	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1150	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210	 GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1270	 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380

Db 1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1389

Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db 1390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1449

Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db 1450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1509

Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db 1510 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1569

Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db 1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1629

Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
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Db 1630 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1689

Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db 1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
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Db 1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1805

Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db 1806 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846

RESULT 12

ADH42302

ID ADH42302 standard; DNA; 2828 BP.

XX

AC ADH42302;

XX

DT 25-MAR-2004 (first entry)

XX

DE Novel human nucleic acid NOV55a.

XX

KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;
 KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;
 KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;
 KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;
 KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
 KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
 KW tissue typing; preventive medicine; pharmacogenomic; vaccine.

XX

OS Homo sapiens.

XX

PN WO2003102159-A2.

XX

PD 11-DEC-2003.
XX
PF 04-JUN-2003; 2003WO-US017573.
XX
PR 04-JUN-2002; 2002US-0385490P.
PR 04-JUN-2002; 2002US-0385615P.
PR 04-JUN-2002; 2002US-0385755P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386355P.
PR 06-JUN-2002; 2002US-0386357P.
PR 06-JUN-2002; 2002US-0386447P.
PR 06-JUN-2002; 2002US-0386459P.
PR 06-JUN-2002; 2002US-0386465P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0386701P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0387078P.
PR 07-JUN-2002; 2002US-0387081P.
PR 07-JUN-2002; 2002US-0387083P.
PR 10-JUN-2002; 2002US-0387429P.
PR 10-JUN-2002; 2002US-0387540P.
PR 10-JUN-2002; 2002US-0387866P.
PR 11-JUN-2002; 2002US-0387606P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387659P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 12-JUN-2002; 2002US-0388432P.
PR 12-JUN-2002; 2002US-0388479P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389604P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390144P.
PR 19-JUN-2002; 2002US-0390209P.
PR 25-JUN-2002; 2002US-0391726P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402268P.
PR 12-AUG-2002; 2002US-0402822P.
PR 13-AUG-2002; 2002US-0403458P.
PR 15-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403732P.
PR 26-AUG-2002; 2002US-0406182P.
PR 12-SEP-2002; 2002US-0410085P.
PR 13-SEP-2002; 2002US-0410505P.
PR 23-SEP-2002; 2002US-0412955P.
PR 30-SEP-2002; 2002US-0415195P.
PR 23-OCT-2002; 2002US-0420627P.

Db	183	 ACAGGGCAGAACAAATGAGTCCTGTTGAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	242
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	243	 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	302
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	303	 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	362
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	363	 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	422
Qy	361	ACCAGCACAAACCACTATTGCGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	423	 ACCAGCACAAACCACTATTGCGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	482
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	483	 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	542
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	543	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	602
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	603	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAACATCTA	662
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	663	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	722
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	723	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	782
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	783	 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	842
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	843	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	902
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	903	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	962
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	963	 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1022
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020

Db	1023	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1082
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1083	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1142
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1143	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1202
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1203	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1262
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1263	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1322
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1323	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1382
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1383	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1442
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1443	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1502
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1503	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1562
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1563	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1622
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1623	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1682
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1683	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1742
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1743	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1802
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Db	1803	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG	1858
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841
Db	1859	GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA	1899

RESULT 13

ABZ33735

ID ABZ33735 standard; cDNA; 2966 BP.

XX

AC ABZ33735;

XX

DT 30-JAN-2003 (first entry)

XX

DE Human TRICH encoding cDNA SEQ ID NO 41.

XX

KW Human; TRICH; transporter and ion channel; transport disorder;
KW cystic fibrosis; diabetes mellitus; Parkinson's disease; cancer;
KW neurological disorder; Alzheimer's disease; Huntington's disease;
KW immunological disorder; AIDS; asthma; cell proliferative disorder;
KW transgenic; gene therapy; neuroprotective; antidiabetic; cytostatic;
KW antiparkinsonian; hypotensive; nootropic; antianaemic; anticonvulsant;
KW cerebroprotective; cardiant; anti-HIV; human immunodeficiency virus;
KW antiasthmatic; antiatherosclerotic; antigout; antiarteriosclerotic;
KW hepatotropic; antiinflammatory; virucide; cytostatic; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200246415-A2.

XX

PD 13-JUN-2002.

XX

PF 05-DEC-2001; 2001WO-US046963.

XX

PR 08-DEC-2000; 2000US-0254303P.

PR 15-DEC-2000; 2000US-0256190P.

PR 21-DEC-2000; 2000US-0257504P.

PR 12-JAN-2001; 2001US-0261546P.

PR 19-JAN-2001; 2001US-0262832P.

PR 26-JAN-2001; 2001US-0264377P.

PR 02-FEB-2001; 2001US-0266019P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Lee EA, Baughn MR, Yue H, Ding L, Raumann BE, Hafalia AJA;
PI Khan FA, Nguyen DB, Elliott VS, Ramkumar J, Walia NK, Ison CH;
PI Lu Y, Gandhi AR, Warren BA, Duggan BM, Tribouley CM, Burford N;
PI Lu DAM, Lal PG, Yao MG, Xu Y, Bruns CM, Thangavelu K, Swarnakar A;
PI Tang YT, Azimzai Y, Thornton M, Arvizu C, Policky JL;

XX

DR WPI; 2002-519667/55.

DR P-PSDB; ABP74104.

XX

PT Novel human transporter and ion channel polypeptide, useful in diagnosis,
PT prevention or treatment of transport, neurological, muscle, immunological
PT and cell proliferative disorders.

XX

PS Claim 96; SEQ ID NO 41; 146pp + Sequence Listing; English.

XX

CC The invention relates to human transporter and ion channel polypeptide
CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-

Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	621	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	680
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	681	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	740
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	741	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	800
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	801	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	860
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	861	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	920
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	921	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	980
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	981	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1040
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1041	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1100
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1101	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1160
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1161	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1220
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1221	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1280
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1281	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1340
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1341	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1400
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1401	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1460

Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1461	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1520
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1521	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1580
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1581	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1640
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1641	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1700
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCTTGTGTGGCCACA	1560
Db	1701	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCTTGTGTGGCCACA	1760
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1761	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1820
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1821	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1880
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1881	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1940
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Db	1941	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG	1996
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841
Db	1997	GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA	2037

RESULT 14

ABN83429

ID ABN83429 standard; DNA; 126512 BP.

XX

AC ABN83429;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein gene.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;

KW spleen; testis; leukocyte; foetal brain; chromosome 14; gene;

KW single nucleotide polymorphism; SNP; ds.

XX

OS Homo sapiens.

XX

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FT	variation	replace(741. .742,C-)
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FT		/note= "This variation is an indel"
FT	variation	replace(2002,T)
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FT	CDS	2010. .124505
FT		/*tag= d
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FT	exon	2010. .3793
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FT		/*tag= ba
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FT	variation	replace(66879,C)
FT		/*tag= bb
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FT	variation	replace(69156,T)
FT		/*tag= bc
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	replace(69280,T)
FT		/*tag= bd

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FT variation replace(70647,T)
FT          /*tag= be
FT          /standard_name= "Single nucleotide polymorphism"
FT variation replace(71867,T)
FT          /*tag= bf
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FT variation replace(71900,T)
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FT variation replace(72369,T)
FT          /*tag= bi

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Query Match          95.7%; Score 1782.8; DB 6; Length 126512;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db          2010 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 2069

Qy          61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||
Db          2070 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 2129

Qy          121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
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Db          2130 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 2189

Qy          181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db          2190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 2249

Qy          241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db          2250 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 2309

Qy          301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy          361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db          2370 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 2429

Qy          421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480
            |||
Db          2430 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 2489

Qy          481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
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Db          2490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 2549

Qy          541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

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Db	2610		CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	2669
Qy	661		CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	2670		CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	2729
Qy	721		TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	2730		TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	2789
Qy	781		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	2790		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	2849
Qy	841		CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
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Qy	901		CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
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Qy	961		AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
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Qy	1021		TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
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Qy	1261		AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
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Qy	1321		AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	3330		AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	3389
Qy	1381		CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440

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Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
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Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
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Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTAT	1786
Db	3750	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGT	3795

RESULT 15

ABX56261

ID ABX56261 standard; DNA; 2813 BP.

XX

AC ABX56261;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1a CG56258-01 DNA SEQ ID 1.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease; ds.

XX

OS Homo sapiens.

XX

PN WO200281625-A2.

XX

PD 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-US010366.

XX

PR 03-APR-2001; 2001US-0281086P.

PR 05-APR-2001; 2001US-0281906P.

PR 06-APR-2001; 2001US-0282020P.

PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.
PR 12-APR-2001; 2001US-0283512P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285381P.
PR 24-APR-2001; 2001US-0286068P.
PR 25-APR-2001; 2001US-0286292P.
PR 07-JUN-2001; 2001US-0296692P.
PR 26-JUN-2001; 2001US-0300883P.
PR 08-AUG-2001; 2001US-0311003P.
PR 13-AUG-2001; 2001US-0311973P.
PR 16-AUG-2001; 2001US-0312901P.
PR 14-SEP-2001; 2001US-0322283P.
PR 05-OCT-2001; 2001US-0327448P.
PR 31-DEC-2001; 2001US-0345734P.
PR 03-JAN-2002; 2002US-0345755P.
PR 04-FEB-2002; 2002US-0354391P.
PR 02-APR-2002; 2002US-00114153.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
PI Mazur A;

XX

DR WPI; 2003-046862/04.

DR P-PSDB; ABU12041.

XX

PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.

XX

PS Claim 3; Page 83-84; 425pp; English.

XX

CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various

CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
 CC syndrome X and wasting disorders associated with chronic diseases and
 CC various cancers. ABX56261-ABX56306 represent the polynucleotide fragments
 CC which encode the NOVX polypeptides represented in ABU12041-ABU12086
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Query Match 95.7%; Score 1782.4; DB 8; Length 2813;
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Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
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Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
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Db	669	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	728
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	729	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	788
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	789	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	848
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Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
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Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1029	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1088
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1089	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1148
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
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Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1209	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1268
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
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Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1329	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1388
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1389	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1448
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1449	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1508
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1509	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1568

Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1569	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1628
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1629	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1688
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1689	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1748
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT	1784
Db	1749	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT	1792

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	2	71.6	3.8	1950	4	US-09-701-068-1		Sequence 1, Appli
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	5	44.8	2.4	2803	4	US-09-701-068-4		Sequence 4, Appli
	6	38.4	2.1	160	1	US-08-182-175A-44		Sequence 44, Appl
	7	38.4	2.1	160	1	US-08-474-633A-53		Sequence 53, Appl
	8	38.4	2.1	160	4	US-08-823-771-53		Sequence 53, Appl
	9	38.4	2.1	160	5	PCT-US92-06412-44		Sequence 44, Appl
c	10	38.4	2.1	2777	3	US-09-310-463-3		Sequence 3, Appli
c	11	38.4	2.1	2777	4	US-08-842-248A-3		Sequence 3, Appli

c	12	37.4	2.0	289	3	US-09-007-005-17	Sequence 17, Appl
c	13	37.4	2.0	289	3	US-09-244-796-17	Sequence 17, Appl
c	14	37.2	2.0	1320	4	US-09-148-545-110	Sequence 110, App
	15	37	2.0	740	4	US-09-270-767-31616	Sequence 31616, A
	16	37	2.0	1600	4	US-09-270-767-15272	Sequence 15272, A
c	17	37	2.0	1890	3	US-08-935-855-19	Sequence 19, Appl
	18	36.8	2.0	160	1	US-08-182-175A-32	Sequence 32, Appl
	19	36.8	2.0	160	1	US-08-182-175A-34	Sequence 34, Appl
	20	36.8	2.0	160	1	US-08-474-633A-29	Sequence 29, Appl
	21	36.8	2.0	160	1	US-08-474-633A-31	Sequence 31, Appl
	22	36.8	2.0	160	4	US-08-823-771-29	Sequence 29, Appl
	23	36.8	2.0	160	4	US-08-823-771-31	Sequence 31, Appl
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c	31	36.8	2.0	2790	4	US-09-546-049-21	Sequence 21, Appl
c	32	36.8	2.0	2922	3	US-09-310-463-1	Sequence 1, Appli
c	33	36.8	2.0	2922	4	US-08-842-248A-1	Sequence 1, Appli
	34	36.6	2.0	289	3	US-09-007-005-17	Sequence 17, Appl
	35	36.6	2.0	289	3	US-09-244-796-17	Sequence 17, Appl
	36	36	1.9	505	4	US-09-621-976-15639	Sequence 15639, A
c	37	36	1.9	1312	4	US-10-140-002-397	Sequence 397, App
c	38	36	1.9	1328	4	US-09-599-360B-46	Sequence 46, Appl
	39	35.6	1.9	189	3	US-09-461-697-213	Sequence 213, App
	40	35.6	1.9	195	3	US-09-461-697-211	Sequence 211, App
	41	35.6	1.9	213	3	US-09-461-697-209	Sequence 209, App
	42	35.6	1.9	231	3	US-09-461-697-207	Sequence 207, App
	43	35.6	1.9	282	3	US-09-461-697-205	Sequence 205, App
	44	35.6	1.9	306	3	US-09-461-697-203	Sequence 203, App
	45	35.6	1.9	696	3	US-09-461-697-193	Sequence 193, App

ALIGNMENTS

RESULT 1

US-09-701-068-3

; Sequence 3, Application US/09701068

; Patent No. 6677506

; GENERAL INFORMATION:

; APPLICANT: Galil, Gad et al.

; TITLE OF INVENTION: DNA CODING FOR A Mg²⁺/H⁺ OR Zn²⁺/H⁺ EXCHANGER AND
TRANSGENIC PLANTS

; TITLE OF INVENTION: EXPRESSING SAME

; FILE REFERENCE: 01/21317

; CURRENT APPLICATION NUMBER: US/09/701,068

; CURRENT FILING DATE: 2001-05-07

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 1935

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(1755)
US-09-701-068-3

Query Match 3.8%; Score 71.6; DB 4; Length 1935;
Best Local Similarity 48.2%; Pred. No. 6.4e-12;
Matches 268; Conservative 0; Mismatches 279; Indels 9; Gaps 2;

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Qy      226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCT 285
      |||| | | ||||| | | || ||| || ||||| ||| ||| ||
Db      253 AGGGGTGTGTTATATTTTCTCGGTCTTGCCTACTGCTTTATTGGGTGTGTCAGCCATCACT 312

Qy      286 GACCGCTTCATGGCATCTATTG---AAGTCATCACCTCTCAAGAGAGGGAGGTGACAATT 342
      | || ||| | ||||| | | ||| | | | | | ||| |||||
Db      313 GCACGGTTCTTCAAGTCTATGGAGAATGTCGTGAAACATTCCCGTAAAGTGGTTACAATT 372

Qy      343 AAGAAACCCAATGGAGAAACCAGCACAACCCTATTTCGGGTCTGGAATGAACTGTCTCC 402
      | | | | | || || || || || || || || || || ||
Db      373 GATCCCATTAATAAGCTGAAGTCATCACATACAAGAAAGTTTGGAACTTTACTATTGCA 432

Qy      403 AACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAG 462
      || | | | |||| | || | || |||| | || || || ||
Db      433 GACATCAGTTTGTGGCGTTTGGAACTAGCTTCCCTCAGATTTCTTTGGCTACCATCGAT 492

Qy      463 GTGTGTGGTCAT-----GGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGG 516
      | | | | | || | | ||||| || || || || || || || ||
Db      493 GCAATACGGAATATGGGGGAGCGGTATGCTGGAGGTCTTGGTCCTGGAACACTTGTGGC 552

Qy      517 AGTGCAGCCTTCAACATGTTTCATCATCATTTGGCATCTGTGTCTACGTGATCCCAGACGGA 576
      || || || | | ||| |||| | | ||||| ||| || |||
Db      553 TCAGCTGCATTTGATCTTTTCCCCATCCACGCTGTTTGTGTGCTTGTGCCAAAAGCTGGA 612

Qy      577 GAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTT 636
      || | | |||| | || || || | | | | || || || ||
Db      613 GAAGTGAAGAAAGATATCCGACTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTGG 672

Qy      637 GCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGG 696
      || ||||| |||| || || || || || || || || || || ||
Db      673 GCTTACATCTGGCTATACATAATCCTCGAGGTGTGGTCACCAAACGTAATTACACTTGTG 732

Qy      697 GAAGGCCTCCTCACTCTCTTCTTCTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGAT 756
      || | | | || | | | | | | | | | | || || || ||
Db      733 GAGGCATTATTGACAGTACTGCAATACGGATTGCTTCTAGTTCATGCGTACGCCCAAGAC 792

Qy      757 AAACGACTGCTCTTCT 772
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Db      793 AAGCGATGGCCTTACT 808
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RESULT 2

US-09-701-068-1

; Sequence 1, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.

; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
 TRANSGENIC PLANTS
 ; TITLE OF INVENTION: EXPRESSING SAME
 ; FILE REFERENCE: 01/21317
 ; CURRENT APPLICATION NUMBER: US/09/701,068
 ; CURRENT FILING DATE: 2001-05-07
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1950
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-701-068-1

Query Match 3.8%; Score 71.6; DB 4; Length 1950;
 Best Local Similarity 48.2%; Pred. No. 6.4e-12;
 Matches 268; Conservative 0; Mismatches 279; Indels 9; Gaps 2;

Qy	226	AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCT	285
Db	258	AGGGGTGTGTTATATTTTCTCGGTCTTGCCTACTGCTTTATTGGGTGTGTCAGCCATCACT	317
Qy	286	GACCGCTTCATGGCATCTATTG---AAGTCATCACCTCTCAAGAGAGGGAGGTGACAATT	342
Db	318	GCACGGTTCCTCAAGTCTATGGAGAATGTCGTGAAACATTCCCGTAAAGTGGTTACAATT	377
Qy	343	AAGAAACCCAATGGAGAAACCAGCACAACTATTTCGGGTCTGGAATGAACTGTCTCC	402
Db	378	GATCCCATTAATAAGCTGAAGTCATCACATACAAGAAAGTTTGGAACTTTACTATTGCA	437
Qy	403	AACCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAG	462
Db	438	GACATCAGTTTGTGGCGTTTGGAACTAGCTTCCCTCAGATTTCTTTGGCTACCATCGAT	497
Qy	463	GTGTGTGGTCAT-----GGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGG	516
Db	498	GCAATACGGAATATGGGGGAGCGGTATGCTGGAGGTCTTGGTCCTGGAACACTTGTGGC	557
Qy	517	AGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGA	576
Db	558	TCAGCTGCATTTGATCTTTTCCCACATCCACGCTGTTTGTGTGCGTTGTGCCAAAAGCTGGA	617
Qy	577	GAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTT	636
Db	618	GAACTGAAAAAGATATCCGACTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTTTGG	677
Qy	637	GCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGG	696
Db	678	GCTTACATCTGGCTATACATAATCCTCGAGGTGTGGTCACCAAACGTAATTACACTTGTG	737
Qy	697	GAAGGCCTCCTCACTCTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGAT	756
Db	738	GAGGCATTATTGACAGTACTGCAATACGGATTGCTTCTAGTTCATGCGTACGCCCAAGAC	797
Qy	757	AAACGACTGCTCTTCT	772
Db	798	AAGCGATGGCCTTACT	813

RESULT 3

US-08-232-463-14

; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match 2.8%; Score 51.6; DB 1; Length 7218;
Best Local Similarity 5.9%; Pred. No. 3.7e-05;
Matches 24; Conservative 215; Mismatches 169; Indels 0; Gaps 0;

Qy 395 CTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCCTCTCTT 454
:: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::


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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
;   APPLICANT: DORNER, F.
;   APPLICANT: SCHEIFLINGER, F.
;   APPLICANT: FALKNER, F. G.
;   TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;   NUMBER OF SEQUENCES: 52
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 1800 Diagonal Road, Suite 500
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22313-0299
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/232,463
;   FILING DATE:
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/07/935,313
;   FILING DATE:
;   APPLICATION NUMBER: EP 91 114 300.6

```

```
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14
```

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Query Match          2.7%; Score 51; DB 1; Length 7218;
Best Local Similarity 3.4%; Pred. No. 5.8e-05;
Matches      9; Conservative 161; Mismatches 91; Indels 0; Gaps 0;
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Qy      1603 GAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGG 1662
          |||| || ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db      1445 GAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1386

Qy      1663 ACATCAGGTGCCC GGGGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAG 1722
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1385 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1326

Qy      1723 GGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACT 1782
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1325 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1266

Qy      1783 GTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGAT 1842
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1265 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1206

Qy      1843 GGGAAAGCCAGTATTGGGTGA 1863
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1205 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1185
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RESULT 5

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US-09-701-068-4
; Sequence 4, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2803
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-701-068-4

Query Match 2.4%; Score 44.8; DB 4; Length 2803;
Best Local Similarity 52.1%; Pred. No. 0.0028;
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy 477 GTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTT 536
||| | | | ||| || ||| || ||| || | | ||
Db 950 GTTTTGTCATATAGGTCTTGGTCCTGGAACACTTGTGGCTCAGCTGCATTTGATCTTTT 1009

Qy 537 CATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCA 596
| |||| | | ||||| ||| || |||| | |||| |
Db 1010 CCCCATCCACGCTGTTTGTGTCGTTGTGCCAAAAGCTGGAGAACTGAAAAAGATATCCGA 1069

Qy 597 TCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATAT 656
|| || | | | | | ||| || | | ||||| || ||
Db 1070 CTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTGGGCTTACATCTGGCTATACAT 1129

Qy 657 GATTCTGGCAGT 668
|| || | ||
Db 1130 AATCCTCGAGGT 1141

RESULT 6

US-08-182-175A-44

; Sequence 44, Application US/08182175A

; Patent No. 5559223

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; APPLICANT: Janet A. Rice

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure
Containing Pro

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/182,175A

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/743,006

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; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axaemethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: E. coli
; CELL TYPE: DH5 alpha
; IMMEDIATE SOURCE:
; CLONE: 82-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..151
; OTHER INFORMATION: /function= "synthetic storage protein"
; OTHER INFORMATION: /product= "protein"
; OTHER INFORMATION: /gene= "ssp"
; OTHER INFORMATION: /standard_name= "7.7.7.7.7.7.5"
US-08-182-175A-44

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Query Match          2.1%; Score 38.4; DB 1; Length 160;
Best Local Similarity 53.3%; Pred. No. 0.042;
Matches 81; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Qy      1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
          | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

Qy      1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

Qy      1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
          | ||| | |||| | ||| | ||| |
Db      124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155

```

RESULT 7

US-08-474-633A-53

; Sequence 53, Application US/08474633A

; Patent No. 5773691

; GENERAL INFORMATION:

; APPLICANT: E. I. DU PONT DE NEMOURS AND

; APPLICANT: COMPANY

; TITLE OF INVENTION: CHIMERIC GENES AND

; TITLE OF INVENTION: METHODS FOR INCREASING

; TITLE OF INVENTION: INCREASING THE LYSINE

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; TITLE OF INVENTION:  AND THREONINE CONTENT
; TITLE OF INVENTION:  OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES:  107
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  E. I. DU PONT DE NEMOURS
;   ADDRESSEE:  AND COMPANY
;   STREET:  1007 MARKET STREET
;   CITY:  WILMINGTON
;   STATE:  DELAWARE
;   COUNTRY:  U.S.A.
;   ZIP:  19898
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  FLOPPY DISK
;   COMPUTER:  IBM PC COMPATIBLE
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/474,633A
;   FILING DATE:
;   CLASSIFICATION:  800
; ATTORNEY/AGENT INFORMATION:
;   NAME:  BARBARA C. SIEGELL
;   REGISTRATION NUMBER:  30,684
;   REFERENCE/DOCKET NUMBER:  BB-1037-C
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  302-992-4931
;   TELEFAX:  302-773-0164
;   TELEX:  835420
; INFORMATION FOR SEQ ID NO:  53:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  160 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (genomic)
;   ORIGINAL SOURCE:
;     STRAIN:  E. coli
;     CELL TYPE:  DH5 alpha
;   IMMEDIATE SOURCE:
;     CLONE:  82-4
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  2..151
;     OTHER INFORMATION:  /function= "synthetic
;     OTHER INFORMATION:  storage protein
;     OTHER INFORMATION:  /product= "protein"
;     OTHER INFORMATION:  /gene= "ssp"
;     OTHER INFORMATION:  /standard_name=
;     OTHER INFORMATION:  "7.7.7.7.7.7.5"
US-08-474-633A-53

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Query Match          2.1%;  Score 38.4;  DB 1;  Length 160;
Best Local Similarity 53.3%;  Pred. No. 0.042;
Matches 81;  Conservative 0;  Mismatches 71;  Indels 0;  Gaps 0;

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Qy      1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
          | |||  |||  | || |  || |  ||  |||| |  || ||  |||  |

```

Db 4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

Qy 1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
 | | | | | | | | | | | | | | | | | | | | | |

Db 64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

Qy 1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
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Db 124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155

RESULT 8

US-08-823-771-53

; Sequence 53, Application US/08823771

; Patent No. 6459019

; GENERAL INFORMATION:

; APPLICANT: E. I. DU PONT DE NEMOURS AND
 ; COMPANY

; TITLE OF INVENTION: CHIMERIC GENES AND
 ; METHODS FOR INCREASING
 ; INCREASING THE LYSINE
 ; AND THREONINE CONTENT

; NUMBER OF SEQUENCES: 107

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS
 ; AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: U.S.A.

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MICROSOFT WORD VERSION 2.0C

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/823,771

; FILING DATE: 24-Mar-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/474,633

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: BARBARA C. SIEGELL

; REGISTRATION NUMBER: 30,684

; REFERENCE/DOCKET NUMBER: BB-1037-C

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 302-992-4931

; TELEFAX: 302-773-0164

; TELEX: 835420

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 160 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

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;      MOLECULE TYPE: DNA (genomic)
;      ORIGINAL SOURCE:
;          STRAIN: E. coli
;          CELL TYPE: DH5 alpha
;      IMMEDIATE SOURCE:
;          CLONE: 82-4
;      FEATURE:
;          NAME/KEY:   CDS
;          LOCATION:   2..151
;          OTHER INFORMATION:  /function= "synthetic
;                               storage protein
;                               /product= "protein"
;                               /gene= "ssp"
;                               /standard_name=
;                               "7.7.7.7.7.7.5"
;      SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-08-823-771-53

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Query Match          2.1%;  Score 38.4;  DB 4;  Length 160;
Best Local Similarity 53.3%;  Pred. No. 0.042;
Matches 81;  Conservative 0;  Mismatches 71;  Indels 0;  Gaps 0;

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Qy      1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
          | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

Qy      1768 AAGAATGATGAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
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Qy      1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
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RESULT 9

PCT-US92-06412-44

; Sequence 44, Application PC/TUS9206412

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; APPLICANT: Janet A. Rice

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure
Containing Pro

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axiomethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: E. coli
; CELL TYPE: DH5 alpha
; IMMEDIATE SOURCE:
; CLONE: 82-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..151
; OTHER INFORMATION: /function= "synthetic storage protein"
; OTHER INFORMATION: /product= "protein"
; OTHER INFORMATION: /gene= "ssp"
; OTHER INFORMATION: /standard_name= "7.7.7.7.7.7.5"
PCT-US92-06412-44

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Best Local Similarity 53.3%; Pred. No. 0.042;
Matches 81; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Qy      1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
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Qy      1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
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Db      64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

Qy      1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
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Db      124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155

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RESULT 10
US-09-310-463-3/c
; Sequence 3, Application US/09310463A
; Patent No. 6384203

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; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM/PC Compatible
; OPERATING SYSTEM: Microsoft Word 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,248A
; FILING DATE: April 24, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 289
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Translation template
;   FEATURE:
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;   OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
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Best Local Similarity 6.5%; Pred. No. 0.13;
Matches 14; Conservative 93; Mismatches 108; Indels 0; Gaps 0;
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Qy      668 TCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTCCAG 727
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Qy      728 TGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACA 787
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; Sequence 17, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
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; EARLIER APPLICATION NUMBER: 60/040,333
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; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 05-Sep-1997
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; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,881

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; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
; LENGTH: 1320
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Db      750 TCCCGGCTGCCAGGGCTCACTTCCAAGCTTACAGAACTCGTGTCACTCATTGTGTGAGCT 691

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Qy      734 TCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTA 773
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Db      630 TCCTTCATCTCAGGCACATAGAAGTCTCCCTGCCSTGCCA 591
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RESULT 15

US-09-270-767-31616

; Sequence 31616, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 31616

; LENGTH: 740

; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-31616

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Matches 109; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	No.	Score	Match	Length					
	1	1863	100.0	1863	13	US-10-054-680-3			Sequence 3, Appli
	2	1784.6	95.8	2766	13	US-10-054-680-1			Sequence 1, Appli
	3	1784.6	95.8	3812	13	US-10-054-680-5			Sequence 5, Appli
	4	1784.4	95.8	2534	15	US-10-256-537-1			Sequence 1, Appli
	5	1784.4	95.8	2534	15	US-10-256-537-3			Sequence 3, Appli
	6	1783	95.7	2781	14	US-10-275-116-1			Sequence 1, Appli
	7	1783	95.7	2782	9	US-09-804-474A-1			Sequence 1, Appli
	8	1782.8	95.7	126512	9	US-09-804-474A-3			Sequence 3, Appli
	9	1782.4	95.7	2813	15	US-10-114-153-1			Sequence 1, Appli
	10	1782.4	95.7	2840	15	US-10-114-153-3			Sequence 3, Appli
	11	1694.8	91.0	2685	15	US-10-114-153-5			Sequence 5, Appli
	12	821.4	44.1	823	15	US-10-029-386-20265			Sequence 20265, A
	13	810.6	43.5	4087	9	US-09-901-419-1			Sequence 1, Appli
	14	785.2	42.1	1836	9	US-09-864-761-16939			Sequence 16939, A
	15	784.8	42.1	5438	18	US-10-357-930-24294			Sequence 24294, A
	16	783.2	42.0	6106	16	US-10-062-674-1648			Sequence 1648, Ap
	17	713.4	38.3	3004	16	US-10-388-934-506			Sequence 506, App
	18	692.4	37.2	4282	14	US-10-281-866-1			Sequence 1, Appli
	19	692.4	37.2	4282	14	US-10-281-866-3			Sequence 3, Appli
	20	503.4	27.0	505	15	US-10-029-386-6536			Sequence 6536, Ap
	21	494	26.5	551	15	US-10-029-386-4103			Sequence 4103, Ap
	22	366	19.6	366	15	US-10-029-386-17804			Sequence 17804, A
	23	334.4	17.9	507	15	US-10-029-386-4003			Sequence 4003, Ap
	24	180	9.7	180	15	US-10-029-386-17706			Sequence 17706, A
	25	164.2	8.8	459	9	US-09-864-761-102			Sequence 102, App
	26	146.6	7.9	1132	15	US-10-369-493-30006			Sequence 30006, A
	27	91.4	4.9	1792	15	US-10-369-493-29835			Sequence 29835, A
	28	79	4.2	477	10	US-09-918-995-2005			Sequence 2005, Ap
	29	79	4.2	1187	15	US-10-243-552-809			Sequence 809, App
c	30	79	4.2	2859	18	US-10-723-860-7370			Sequence 7370, Ap
	31	77.4	4.2	1248	18	US-10-425-115-125495			Sequence 125495,
	32	71.6	3.8	1617	9	US-09-938-842A-2591			Sequence 2591, Ap
	33	71.6	3.8	1617	11	US-09-938-842A-2591			Sequence 2591, Ap
	34	58.2	3.1	862	16	US-10-424-599-86000			Sequence 86000, A
c	35	57.4	3.1	173	18	US-10-674-124A-2603			Sequence 2603, Ap
	36	45.2	2.4	1487	17	US-10-437-963-77130			Sequence 77130, A
	37	41.2	2.2	55005	18	US-10-719-993-6968			Sequence 6968, Ap
c	38	41.2	2.2	318760	18	US-10-719-993-6765			Sequence 6765, Ap
	39	39.6	2.1	1635	16	US-10-282-122A-29169			Sequence 29169, A
	40	39.6	2.1	30306	13	US-10-087-192-523			Sequence 523, App
c	41	39	2.1	77922	17	US-10-741-601-5674			Sequence 5674, Ap
	42	39	2.1	203127	17	US-10-741-601-5654			Sequence 5654, Ap
	43	38.8	2.1	244	18	US-10-674-124A-612			Sequence 612, App
	44	38.8	2.1	2318	17	US-10-437-963-21282			Sequence 21282, A
	45	38.8	2.1	2967	17	US-10-437-963-21285			Sequence 21285, A

ALIGNMENTS

RESULT 1

US-10-054-680-3

; Sequence 3, Application US/10054680

; Publication No. US20020132998A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-680-3

Query Match 100.0%; Score 1863; DB 13; Length 1863;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTCCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATTCCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540

Db	481	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCACTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCACTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380

Db 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
 Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
 |||||
 Db 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
 Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
 |||||
 Db 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
 Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
 |||||
 Db 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
 Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
 |||||
 Db 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
 Qy 1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
 |||||
 Db 1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
 Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 |||||
 Db 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
 |||||
 Db 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
 Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860
 |||||
 Db 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860
 Qy 1861 TGA 1863
 |||
 Db 1861 TGA 1863

RESULT 2

US-10-054-680-1

; Sequence 1, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. US20020132998A1e1 Human Ion Exchanger Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0301-USA

; CURRENT APPLICATION NUMBER: US/10/054,680

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,384

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2766
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-680-1

Query Match 95.8%; Score 1784.6; DB 13; Length 2766;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720

Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620


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Db      1561 |TTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT| 1620
Qy      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
Db      1621 |TTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT| 1680
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
Db      1681 |ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT| 1740
Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
Db      1741 |GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA| 1800
Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
Db      1797 |GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA| 1841
Db      1797 GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

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RESULT 3

US-10-054-680-5

; Sequence 5, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0301-USA

; CURRENT APPLICATION NUMBER: US/10/054,680

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,384

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 3812

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-054-680-5

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Query Match          95.8%; Score 1784.6; DB 13; Length 3812;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
Db      618 |ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC| 677
Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
Db      678 |TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC| 737
Qy      121 ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180

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Db	738	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	797
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	798	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	857
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	858	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	917
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	918	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	977
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	978	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	1037
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	1038	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	1097
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC	540
Db	1098	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC	1157
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1158	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1217
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1218	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1277
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1278	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1337
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1338	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1397
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1398	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1457
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1458	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1517
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1518	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1577
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1578	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1637

Qy	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1638	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1697
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1698	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1757
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1758	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1817
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1818	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1877
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1878	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1937
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1938	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1997
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1998	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2057
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2058	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2117
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCTTGTGTGGCCACA	1560
Db	2118	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCTTGTGTGGCCACA	2177
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	2178	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	2237
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	2238	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	2297
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2298	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2357
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA	1800
Db	2358	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG	2413
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841
Db	2414	GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA	2454

RESULT 4

US-10-256-537-1

; Sequence 1, Application US/10256537
 ; Publication No. US20030162196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carroll, Joseph M.
 ; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
 ; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER
 ; FILE REFERENCE: MPI01-231P1RM
 ; CURRENT APPLICATION NUMBER: US/10/256,537
 ; CURRENT FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/325,737
 ; PRIOR FILING DATE: 2001-09-28
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 2534
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-256-537-1

Query Match 95.8%; Score 1784.4; DB 15; Length 2534;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	343	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	402
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	403	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	462
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	463	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	522
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	523	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	582
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	583	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	642
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	643	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	702
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	703	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	762
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	763	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	822

Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	823	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	882
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	883	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	942
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	943	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1002
Qy	661	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	1003	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	1062
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1063	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1122
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1123	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1182
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1183	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1242
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1243	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1302
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1303	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1362
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1363	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1422
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1423	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1482
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1483	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1542
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1543	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1602
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1603	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1662

Qy 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
 |||
 Db 1663 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722

Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
 |||
 Db 1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
 |||
 Db 1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842

Qy 1501 GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
 |||
 Db 1843 GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1902

Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
 |||
 Db 1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1962

Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
 |||
 Db 1963 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 2022

Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 |||
 Db 2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
 |||
 Db 2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128

RESULT 5

US-10-256-537-3

; Sequence 3, Application US/10256537
 ; Publication No. US20030162196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carroll, Joseph M.
 ; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
 ; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER
 ; FILE REFERENCE: MPI01-231P1RM
 ; CURRENT APPLICATION NUMBER: US/10/256,537
 ; CURRENT FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/325,737
 ; PRIOR FILING DATE: 2001-09-28
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 2534
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (343)...(2130)

US-10-256-537-3

Query Match 95.8%; Score 1784.4; DB 15; Length 2534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
      |||
Db    343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
      |||
Db    403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy     121 ACAGGGCAGAACAATGAGTCCTGTT CAGGGTCATCGGACTGCAAGGAGGGTGT CATCCTG 180
      |||
Db    463 ACAGGGCAGAACAATGAGTCCTGTT CAGGGTCATCGGACTGCAAGGAGGGTGT CATCCTG 522

Qy     181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
      |||
Db    523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy     241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTTGCTGACCGCTTCATGGCA 300
      |||
Db    583 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTTGCTGACCGCTTCATGGCA 642

Qy     301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
      |||
Db    643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy     361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420
      |||
Db    703 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy     421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC 480
      |||
Db    763 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC 822

Qy     481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
      |||
Db    823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 882

Qy     541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
      |||
Db    883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy     601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
      |||
Db    943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy     661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
      |||
Db   1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy     721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
      |||
Db   1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy     781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db	1123	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1182
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1183	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1242
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1243	 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1302
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1303	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1362
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1363	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1422
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1423	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1482
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1483	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1542
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1543	 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1602
Qy	1261	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1603	 AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1662
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1663	 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1722
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1723	 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1782
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1783	 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1842
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1843	 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1902
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1903	 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1962
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680


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Db      1963  GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 2022
Qy      1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
          |||
Db      2023  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082
Qy      1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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Db      2083  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128

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RESULT 6

US-10-275-116-1

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; Sequence 1, Application US/10275116
; Publication No. US20030096312A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: No. US20030096312A1el natrium-calium exchanger protein
; FILE REFERENCE: HNCX3CWWS
; CURRENT APPLICATION NUMBER: US/10/275,116
; CURRENT FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2781)
US-10-275-116-1

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Query Match          95.7%; Score 1783; DB 14; Length 2781;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy      1  ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
          |||
Db      1  ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
Qy     61  TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
          |||
Db     61  TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
Qy    121  ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180
          |||
Db    121  ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180
Qy    181  CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
          |||
Db    181  CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
Qy    241  TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
          |||
Db    241  TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
Qy    301  TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Db	301	 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAAACCACTATTCTGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	 ACCAGCACAAACCACTATTCTGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTCCTACATCTGGCTCTATATGATT	660
Db	601	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200

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Db      1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
Qy      1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
        |||
Db      1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
Qy      1261 AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCCTGCC 1320
        . |||
Db      1261 AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCCTGCC 1320
Qy      1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
        |||
Db      1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
Qy      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
        |||
Db      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
        |||
Db      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
        |||
Db      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
        |||
Db      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
Qy      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
        |||
Db      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
        |||
Db      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
        |||
Db      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796
Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
        | | | | | | | | | | | | | | | | | | | | | |
Db      1797 GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

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RESULT 7

US-09-804-474A-1

; Sequence 1, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000891
; CURRENT APPLICATION NUMBER: US/09/804,474A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Human
US-09-804-474A-1

Query Match 95.7%; Score 1783; DB 9; Length 2782;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 189

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249

Qy    241 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 309

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369

Qy    361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 429

Qy    421 CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 489

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 549

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 609

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db	610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	669
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	670	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	729
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	730	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	909
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	910	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC	969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1030	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1450	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1509

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Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
          |||
Db      1510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1569

Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
          |||
Db      1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1629

Qy      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
          |||
Db      1630 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1689

Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
          |||
Db      1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
          |||
Db      1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1805

Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
          |||
Db      1806 GGTAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846

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RESULT 8

US-09-804-474A-3

; Sequence 3, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000891

; CURRENT APPLICATION NUMBER: US/09/804,474A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 126512

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(126512)

; OTHER INFORMATION: n = A,T,C or G

US-09-804-474A-3

Query Match 95.7%; Score 1782.8; DB 9; Length 126512;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db	2010	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	2069
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	2070	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	2129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	2130	ACAGGGCAGAACAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	2189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	2190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	2249
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	2250	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	2309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	2310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	2369
Qy	361	ACCAGCACAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	2370	ACCAGCACAACAACCTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	2429
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	2430	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	2489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	2490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	2549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	2550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	2609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	2610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	2669
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	2670	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	2729
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	2730	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	2789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	2790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	2849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	2850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	2909

Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	2910	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	2969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	2970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	3029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	3030	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	3089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	3090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	3149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	3150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	3209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	3210	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	3269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	3270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	3329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	3330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	3389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	3390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	3449
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	3450	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	3509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	3510	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	3569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	3570	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	3629
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	3630	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	3689
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	3690	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	3749


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; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 1
; LENGTH: 2813
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(2793)
US-10-114-153-1
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Query Match          95.7%; Score 1782.4; DB 15; Length 2813;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 68

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 128

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 188

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 248

Qy    241 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 308

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 368

Qy    361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 428

Qy    421 CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 488

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 548
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Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	549	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	608
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCCTACATCTGGCTCTATATGATT	660
Db	609	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCCTACATCTGGCTCTATATGATT	668
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	669	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	728
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	729	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	788
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	789	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	848
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	849	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	908
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	909	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	968
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	969	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1028
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1029	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1088
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1089	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1148
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1149	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1208
Qy	1201	GACCCATGTTCTTACCACTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1209	GACCCATGTTCTTACCACTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1268
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1269	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1328
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1329	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1388

Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
 |||
 Db 1389 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1448
 Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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 Db 1449 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1508
 Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
 |||
 Db 1509 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1568
 Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
 |||
 Db 1569 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1628
 Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
 |||
 Db 1629 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1688
 Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 |||
 Db 1689 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1748
 Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGT 1784
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 Db 1749 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGT 1792

RESULT 10

US-10-114-153-3

; Sequence 3, Application US/10114153
 ; Publication No. US20030185815A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Mezes, Peter
 ; APPLICANT: Smithson, Glennnda
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Li, Li
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Gangolli, Esha
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Taupier, Raymond J. Jr.
 ; APPLICANT: Heyes, Melvyn
 ; APPLICANT: Ju, Jingfang
 ; APPLICANT: Peyman, John

```

; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 3
; LENGTH: 2840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(2838)
US-10-114-153-3

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Query Match          95.7%; Score 1782.4; DB 15; Length 2840;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 122

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      123 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 182

Qy      121 ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      183 ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 242

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Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	243	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	302
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	303	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	362
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	363	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	422
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	423	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	482
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	483	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	542
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	543	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	602
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	603	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	662
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	663	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	722
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	723	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	782
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	783	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	842
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	843	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	902
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	903	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	962
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	963	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1022
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1023	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1082

Qy	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1083	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1142
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1143	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1202
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1203	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1262
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1263	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1322
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1323	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1382
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1383	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1442
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1443	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1502
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1503	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1562
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1563	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1622
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1623	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1682
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1683	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1742
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1743	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1802
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT	1784
Db	1803	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT	1846

RESULT 11

US-10-114-153-5

; Sequence 5, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251


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; SEQ ID NO 5
;   LENGTH: 2685
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2685)
US-10-114-153-5
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Qy	746	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	805
Db	662	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	721
Qy	806	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	865
Db	722	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	781
Qy	866	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG	925
Db	782	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG	841
Qy	926	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	985
Db	842	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	901
Qy	986	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAACAGA	1045
Db	902	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAACAGA	961
Qy	1046	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1105
Db	962	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1021
Qy	1106	TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1165
Db	1022	TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1081
Qy	1166	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1225
Db	1082	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1141
Qy	1226	AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA	1285
Db	1142	AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA	1201
Qy	1286	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1345
Db	1202	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1261
Qy	1346	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1405
Db	1262	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1321
Qy	1406	TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1465
Db	1322	TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1381
Qy	1466	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1525
Db	1382	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1441
Qy	1526	CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1585
Db	1442	CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1501
Qy	1586	CAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGTGTTATGG	1645

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Db      1502 CAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGTGTATGG 1561
Qy      1646 AGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGTACAGTCATCGTCCCCCTTTAGGACAG 1705
                |||
Db      1562 AGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGTACAGTCATCGTCCCCCTTTAGGACAG 1621
Qy      1706 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1765
                |||
Db      1622 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1681
Qy      1766 TCAAGAATGATGAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCC 1825
                |||
Db      1682 TCAAGAATGATGAAAC---TGTGAAAACCATAAGGGTTAAATAGTAGATGAGGAGGAA 1737
Qy      1826 AAGAGGATAGCAGAGA 1841
                |||
Db      1738 TACGAAAGGCAAGAGA 1753

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RESULT 12

US-10-029-386-20265

; Sequence 20265, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE

; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 20265

; LENGTH: 823

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AL160191.1

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

; OTHER INFORMATION: SWISSPROT HIT: P57103, EVALUE 0.00e+00

; OTHER INFORMATION: EST_HUMAN HIT: BI913344.1, EVALUE 0.00e+00

; OTHER INFORMATION: NT HIT: gi15147253, EVALUE 0.00e+00

US-10-029-386-20265

Query Match 44.1%; Score 821.4; DB 15; Length 823;

Best Local Similarity 99.9%; Pred. No. 1.2e-255;

Matches 822; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      432 TGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGA 491
                |||
Db      1 TGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGA 60

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Qy	492	TCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCAT	551
Db	61	TCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCAT	120
Qy	552	CTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTT	611
Db	121	CTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTT	180
Qy	612	CATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTT	671
Db	181	CATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTT	240
Qy	672	CTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTCCAGTGTG	731
Db	241	CTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTCCAGTGTG	300
Qy	732	TGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAA	791
Db	301	TGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAA	360
Qy	792	GTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGG	851
Db	361	GTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGG	420
Qy	852	CATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAACCTGGTGCCCCCT	911
Db	421	CATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAACCTGGTGCCCCCT	480
Qy	912	GGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAA	971
Db	481	GGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAA	540
Qy	972	GCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCT	1031
Db	541	GCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCT	600
Qy	1032	TTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGG	1091
Db	601	TTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGG	660
Qy	1092	TGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAG	1151
Db	661	TGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAG	720
Qy	1152	CGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTC	1211
Db	721	CGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTC	780
Qy	1212	TTACCAAGTGCCTGGGAACTGTGGGGCTGTACTCCTGACAGTG	1254
Db	781	TTACCAAGTGCCTGGGAACTGTGGGGCTGTACTCCTGACAGTG	823

RESULT 13

US-09-901-419-1

; Sequence 1, Application US/09901419

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; Patent No. US20020069421A1
; GENERAL INFORMATION:
; APPLICANT: The Curators of the University of Missouri
; TITLE OF INVENTION: LARGE SCALE EXPRESSION AND PURIFICATION OF RECOMBINANT
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: UMO1531.1
; CURRENT APPLICATION NUMBER: US/09/901,419
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/218,125
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4087
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (268)..(3180)
; NAME/KEY: sig_peptide
; LOCATION: (268)..(363)
; NAME/KEY: misc_feature
; LOCATION: (3178)
; OTHER INFORMATION: A Poly (H) affinity tag comprising 6 His residues
; OTHER INFORMATION: have been inserted at the C-Terminus end of the
; OTHER INFORMATION: coding region of the protein
US-09-901-419-1

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Query Match          43.5%; Score 810.6; DB 9; Length 4087;
Best Local Similarity 68.5%; Pred. No. 9.8e-252;
Matches 1211; Conservative 0; Mismatches 519; Indels 39; Gaps 5;

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Qy      46 TTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCA 105
      |||  || | || | |||  || || | | | | | |||
Db      307 TTTCACGTGATAGCCATGGTGGCTCTCTTGTTTTCCCATGTGGACCATATAAGTGCTGAG 366

Qy      106 GGGGACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAG 165
      || || | | || | | | | || | | | | ||| |||
Db      367 ACAGAAATGGAAGGAGAAGGCAACGAGACTGGCGAGTGTACTGGCTCCTATTACTGTAAG 426

Qy      166 GAGGGTGTTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCC 225
      |||| || || | || || ||| | || | ||||| |||| ||||| |||||
Db      427 AAGGGGGTGATTTTACCCATTTGGGAGCCCCAGGACCCTTCCTTTGGAGACAAAATTGCT 486

Qy      226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCT 285
      || | | ||| ||||| ||||| || | ||||| ||||| || | ||||| |||||
Db      487 AGAGCGACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCAATCATTGCT 546

Qy      286 GACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAG 345
      ||||| ||||| | ||||| ||||| ||||| ||||| || | || | |||
Db      547 GACCGGTTTCATGTCCTCTATAGAAGTCATCACGTCTCAAGAGAAAGAAATCACCATAAAG 606

Qy      346 AAACCCAATGGAGAAACCAGCACAACTTATTCGGGTCTGGAATGAACTGTCTCCAAC 405
      ||||| ||||| |||| | | || || | | ||||| || | || |||||
Db      607 AAACCCAATGGAGAGACCACCAAGACAACGTGTGAGGATCTGGAATGAGACAGTGTCCAAC 666

Qy      406 CTGACCCTTATGGCCCTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTG 465

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Db	667	CTGACCTTGATGGCCCTGGGGTCTTCAGCTCCAGAGATTCTCCTTTCAGTAATCGAGGTG	726
Qy	466	TGTGGTCATGGGTTTATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCC	525
Db	727	TGTGGCCATAACTTCACTGCAGGAGACCTTGGCCCTAGCACCATCGTGGGGAGTGCTGCA	786
Qy	526	TTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGC	585
Db	787	TTCAACATGTTTCATCATCATTGCCCTTTGTGTGTATGTCGTCCCGGATGGGGAGACAAGG	846
Qy	586	AAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATC	645
Db	847	AAGATCAAGCATCTGCGTGTGTTCTTTGTGACAGCAGCATGGAGCATCTTTGCCTATACC	906
Qy	646	TGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTC	705
Db	907	TGGCTTTACATCATTTTGTCTGTCTAGCTCCCCTGGGGTTCGTGGAGGTCTGGGAAGGTTTG	966
Qy	706	CTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTG	765
Db	967	CTTACTTTCTTCTTCTTCCCCATCTGCGTTGTGTTTGCTTGGGTGGCAGACAGGAGGCTT	1026
Qy	766	CTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATA	825
Db	1027	CTGTTTTACAAGTATGTCTACAAGAGGTATCGGGCTGGCAAGCAGAGGGGAATGATTATT	1086
Qy	826	GAGACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATG	876
Db	1087	GAACACGAAGGAGACAGGCCATCTTCCAAGACAGAAATTGAAATGGATGGGAAAGTGGTC	1146
Qy	877	AATTCCCA-----TTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAG-----	921
Db	1147	AATTCCCATGTTGACAGTTTCTTAGATGGAGCCCTGGTTCTGGAGGTTGATGAGAGGGAC	1206
Qy	922	---GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAA	978
Db	1207	CAAGATGATGAAGAAGCCAGGCGAGAAATGGCTAGGATTCTGAAGGAACCTCAAGCAGAAG	1266
Qy	979	CACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCAC	1038
Db	1267	CATCCAGAGAAGGAAATAGAGCAATTAATAGAATTAGCCAATTACCAAGTCTTAAGTCAG	1326
Qy	1039	CAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGC	1098
Db	1327	CAGCAAAAAAGTCGAGCGTTTTACCGTATTCAAGCTACCCGCCTGATGACCGGAGCAGGC	1386
Qy	1099	AATATCCTGAAGAAACATGCAGCAGAACCAAGCAAGAAGGCCTCCAGCATGAGCGAGGTG	1158
Db	1387	AACATTTTAAAGAGGCATGCAGCAGACCAAGCCAGGAAAGCTGTGAGCATGCATGAGGTC	1446
Qy	1159	CACACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC	1215
Db	1447	AACACGGAAGTGGCTGAAAATGACCCTGTGAGTAAGATCTTCTTTGAACAAGGGACATAT	1506
Qy	1216	CAGTGCCTGGGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATG	1275

Db	1507	CAGTGTCTGGAGA ACTGTGGCACAGTAGCCCTGACCATATATCCGCAGAGGTGGTGATT TG	1566
Qy	1276	TCAAAGACC ATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC	1335
Db	1567	ACCAAACTGTGTTT GTTGACTTCAGAACAGAGGATGGCAGCCAATGCTGGATCTGAT	1626
Qy	1336	TATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC	1395
Db	1627	TACGAATTTACCGAAGGA ACTGTGGTCTTTAAGCCTGGTGAGACCCAGAAGGAAATCAGA	1686
Qy	1396	GTGGGCATAATTGATGACGACATTTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC	1455
Db	1687	GTTGGCATCATTGATGATGACATCTTTGAGGAGGATGAGAATTTCTTGTGCATCTCAGC	1746
Qy	1456	AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT	1515
Db	1747	AACGTCAAAGTATCTTTGGAAGCCTCGGAAGACGGCATCCTGGAAGC-----CAGT	1797
Qy	1516	CTTCCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT	1575
Db	1798	CATGTCTCTACCCTTGCTTGCTGGGATCCCCCTCCACTGCCACCGTGACTATTTTTGAT	1857
Qy	1576	GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTGAGTGAGAGTATT	1635
Db	1858	GATGACCATGCTGGCATCTTTACTTTTGAGGAACCGGTGACTCATGTGAGTGAGAGCATT	1917
Qy	1636	GGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCC	1695
Db	1918	GGCATCATGGAGGTGAAAGTTCTGAGAACATCTGGAGCACGTGGAAATGTTATCGTTCCC	1977
Qy	1696	TTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGG	1755
Db	1978	TATAAGACCATTGAGGGGACCGCCAGAGGTGGAGGGGAGGACTTTGAGGACACATGCGGA	2037
Qy	1756	GAGTTGGAATTCAAGAATGATGAAACTGT	1784
Db	2038	GAGCTCGAGTTCCAGAATGACGAAATTGT	2066

; PRIOR APPLICATION NUMBER: US 60/207,456

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16939
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007281.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
; OTHER INFORMATION: NT HIT: X91213.1, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AW452398.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P32418, EVALUE 0.00e+00
US-09-864-761-16939

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Query Match          42.1%; Score 785.2; DB 9; Length 1836;
Best Local Similarity 68.3%; Pred. No. 1.1e-243;
Matches 1166; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

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Qy	109	GACGTGCCAAGCACAGGGCAGAAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAG	168
Db	133	GAAATGGAAGGAGAAGGAAATGAAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA	192
Qy	169	GGTGTTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG	228
Db	193	GGGGTGATTTTGCCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA	252
Qy	229	GTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGAC	288
Db	253	GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT	312
Qy	289	CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGGAGGTGACAATTAAGAAA	348
Db	313	CGGTTTCATGTCTCTATAGAAGTCATCACATCTCAAGAAAAAGAAATAACCATAAAGAAA	372
Qy	349	CCCAATGGAGAAAACCAGCACAACTTATTCGGGTCTGGAATGAACTGTCTCCAACCTG	408
Db	373	CCCAATGGAGAGACCACCAAGACAACCTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG	432
Qy	409	ACCCTTATGGCCCTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT	468
Db	433	ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTTCAGTAATTGAAGTGTGT	492
Qy	469	GGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC	528
Db	493	GGCCATAACTTCACTGCAGGAGACCTCGGTCTAGCACCATCGTGGGAAGTGTCTGCATTC	552
Qy	529	AACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAG	588
Db	553	AATATGTTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG	612
Qy	589	ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG	648
Db	613	ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG	672
Qy	649	CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC	708
Db	673	CTTTACATTATTTTGTCTGTCTATCTCCTGGTGTGTGGAGGTCTGGGAAGGTTTGCTT	732
Qy	709	ACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC	768
Db	733	ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTTCGCTTGGGTAGCGGATAGGAGACTTCTG	792
Qy	769	TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG	828
Db	793	TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA	852
Qy	829	ACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATGAAT	879
Db	853	CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT	912
Qy	880	TCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAG-----	921
Db	913	TCTCATGTTGAAAATTTCTTAGATGGTGCTCTGGTTCTGGAGGTGGATGAGAGGGACCAA	972
Qy	922	GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC	981

Db 973 GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACCTAAGCAGAAGCAT 1032
 Qy 982 CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAA 1041
 Db 1033 CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG 1092
 Qy 1042 CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT 1101
 Db 1093 CAAAAAAGTAGAGCATTTTATCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC 1152
 Qy 1102 ATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC 1161
 Db 1153 ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTGAGCATGCACGAGGTCAAC 1212
 Qy 1162 ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG 1218
 Db 1213 ACTGAAGTGACTGAAAATGACCCTGTTAGTAAGATCTTCTTTGAACAAGGGACATATCAG 1272
 Qy 1219 TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCA 1278
 Db 1273 TGTCTGGAGAACTGTGGTACTGTGGCCCTTACCATTATCCGCAGAGGTGGTGATTTGACT 1332
 Qy 1279 AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT 1338
 Db 1333 AACACTGTGTTTGTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT 1392
 Qy 1339 GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG 1398
 Db 1393 GAATTTACTGAAGGAACTGTGGTGTTTAAGCCTGGTGATACCCAGAAGGAAATCAGAGTG 1452
 Qy 1399 GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT 1458
 Db 1453 GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTTCTTGTGCATCTCAGCAAT 1512
 Qy 1459 GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT 1518
 Db 1513 GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC-----CAATCAT 1563
 Qy 1519 CCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGAT 1578
 Db 1564 GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACATTTTTTGATGAT 1623
 Qy 1579 GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTGATGTCAGTGAGAGTATTGGT 1638
 Db 1624 GACCACGCAGGCATTTTTACTTTTGAAGAACCTGTGACTCATGTGAGTGAGAGCATTGGC 1683
 Qy 1639 GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTT 1698
 Db 1684 ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT 1743
 Qy 1699 AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAG 1758
 Db 1744 AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTTGAGGACACTTGTGGAGAG 1803
 Qy 1759 TTGAATTCAAGAATGATGAAACTGTAT 1786

Db 365 GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT 424
 Qy 289 CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA 348
 || ||||| | |||| ||||| ||||| ||||| | || | || |||||
 Db 425 CGGTTTCATGTCCTCTATAGAAGTCATCACATCTCAAGAAAAAGAAATAACCATAAAGAAA 484
 Qy 349 CCCAATGGAGAAACCAGCACAACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTG 408
 ||||| |||| | || || || || || || ||||| ||||| || |||||
 Db 485 CCCAATGGAGAGACCACCAAGACAACCTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG 544
 Qy 409 ACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT 468
 ||| | ||||| || || ||||| ||||| |||| | ||||| |||||
 Db 545 ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTCAGTAATTGAAGTGTGT 604
 Qy 469 GGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC 528
 || ||| |||| ||| || || || || || |||| | || | |||| | |||
 Db 605 GGCCATAACTTCACCTGCAGGAGACCTCGGTCCCTAGCACCATCGTGGGAAGTGTGCATTTC 664
 Qy 529 AACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG 588
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 Db 665 AATATGTTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG 724
 Qy 589 ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTGCCTACATCTGG 648
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 Db 725 ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTGCCTACACCTGG 784
 Qy 649 CTCTATATGATTCTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC 708
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 Db 785 CTTTACATTATTTTGTCTGTCATATCTCCTGGTGTGTGGAGGTCTGGGAAGGTTTGCTT 844
 Qy 709 ACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC 768
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 Db 845 ACTTCTCTTCTTCTTTCCCATCTGTGTTGTGTTTCGCTTGGGTAGCGGATAGGAGACTTCTG 904
 Qy 769 TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG 828
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 Db 905 TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA 964
 Qy 829 ACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATGAAT 879
 || || || || || || || || || || || || || || || || || || ||
 Db 965 CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT 1024
 Qy 880 TCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAG----- 921
 || ||| || || || || || || || || || || || || || || || ||
 Db 1025 TCTCATGTTGAAAATTTCTTAGATGGTGCTCTGGTTCTGGAGGTGGATGAGAGGGACCAA 1084
 Qy 922 GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC 981
 || | || || | || |||| || ||||| ||||| || ||||| || ||
 Db 1085 GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACCTTAAGCAGAAGCAT 1144
 Qy 982 CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTCCCACCAA 1041
 ||||| || || |||| || | || || || || || || || || || ||
 Db 1145 CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG 1204
 Qy 1042 CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT 1101
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 Db 1205 CAAAAAAGTAGAGCATTTTATCGCATTCAGCTACTCGCCTCATGACTGGAGCTGGCAAC 1264

